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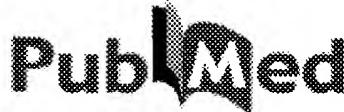
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PMID: 9483985 [PubMed - indexed for MEDLINE]

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PMID: 9119220 [PubMed - indexed for MEDLINE]

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Tanpakushitsu Kakusan Koso. 1997 Feb;42(3 Suppl):571-6. Review. Japanese. No abstract available.
PMID: 9163000 [PubMed - indexed for MEDLINE]

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Curr Opin Genet Dev. 1996 Aug;6(4):469-74. Review.
PMID: 8791530 [PubMed - indexed for MEDLINE]

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Curr Top Microbiol Immunol. 1996;212:229-38. Review. No abstract available.
PMID: 8934822 [PubMed - indexed for MEDLINE]

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Tanpakushitsu Kakusan Koso. 1995 Jul;40(9):1100-14. Review. Japanese. No abstract available.
PMID: 7667497 [PubMed - indexed for MEDLINE]

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 Axon guidance: a compelling case for repelling growth cones.
Cell. 1995 May 19;81(4):471-4. Review. No abstract available.
PMID: 7758101 [PubMed - indexed for MEDLINE]

 **91:** [Keynes RJ, Cook GM.](#) [Related Articles](#), [Links](#)

 Repulsive and inhibitory signals.
Curr Opin Neurobiol. 1995 Feb;5(1):75-82. Review.
PMID: 7539649 [PubMed - indexed for MEDLINE]

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Curr Opin Genet Dev. 1994 Aug;4(4):596-601. Review.
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```
=> s human semaphorin
 20 FILES SEARCHED...
 22 FILES SEARCHED...
 44 FILES SEARCHED...
 63 FILES SEARCHED...
L1      1139 HUMAN SEMAPHORIN
```

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=> DUP REM L1
DUPLICATE IS NOT AVAILABLE IN 'ADISINSIGHT, ADISNEWS, BIOCOMMERCE, DGENE,
DRUGMONOG2, IMSRESEARCH, FEDRIP, FOREGE, GENBANK, IMSPRODUCT, KOSMET,
MEDICONF, NUTRACEUT, PCTGEN, PHAR, PHARMAML, RDISCLOSURE, SYNTHLINE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L1
```

L2 967 DUP REM L1 (172 DUPLICATES REMOVED)

=> S semaphorin 6A OR semaphorin 6A-1 OR semaphorin VIA

22 FILES SEARCHED...

49 FILES SEARCHED...

L3 114 SEMAPHORIN 6A OR SEMAPHORIN 6A-1 OR SEMAPHORIN VIA

=> DUP REM L3

DUPLICATE IS NOT AVAILABLE IN 'ADISINSIGHT, ADISNEWS, BIOCOMMERCE, DGENE, DRUGMONOG2, IMSRESEARCH, FEDRIP, FOREGE, GENBANK, IMSPRODUCT, KOSMET, MEDICONF, NUTRACEUT, PCTGEN, PHAR, PHARMAML, RDISCLOSURE, SYNTHLINE'.

ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE

PROCESSING COMPLETED FOR L3

L4 86 DUP REM L3 (28 DUPLICATES REMOVED)

=> D L4 1-86

L4 ANSWER 1 OF 86 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

AN 2004:119870 CAPLUS

DN 140:158649

TI Sequence homologs of signaling and adhesion proteins from human with possible therapeutic uses and cDNAs encoding them

IN Alsobrook, John; Anderson, David; Boldog, Ferenc; Burgess, Catherine; Casman, Stacie; Edinger, Shlomit R.; Gerlach, Valerie; Grosse, William; Guo, Xiaojia; Gusev, Vladimir; Ji, Weizhen; Larochelle, William; Lepley, Denise; Li, Li; Liu, Xiaohong; MacDougall, John R.; Malyankar, Uriel M.; Millet, Isabelle; Padigaru, Muralidhara; Patturajan, Meera; Peyman, John A.; Rastelli, Luca; Rieger, Daniel; Rothenberg, Mark E.; Shimkets, Richard; Stone, David J.; Taupier, Raymond; Vernet, Corine; Zerhusen, Bryan

PA USA

SO U.S. Pat. Appl. Publ., 199 pp., Cont.-in-part of U.S. Ser. No. 520,781.
CODEN: USXXCO

DT Patent

LA English

FAN.CNT 139

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004029150	A1	20040212	US 2003-403676	20030331
	US 6689866	B1	20040210	US 2000-520781	20000308
	WO 2003085096	A2	20031016	WO 2003-US9929	20030401
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG		
	WO 2003102584	A2	20031211	WO 2003-US17412	20030530
	WO 2003102584	A3	20040219		
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PRAI	US 2004018977	A1	20040129	US 2003-449548	20030530
	US 1999-123667P	P	19990309		
	US 2000-520781	A2	20000308		
	US 2002-368996P	P	20020401		
	US 2002-369980P	P	20020404		
	US 2002-370381P	P	20020405		
	US 2002-370969P	P	20020408		
	US 2002-371002P	P	20020409		
US 2002-372002P	P	20020412			
US 2002-384297P	P	20020530			
US 2002-384798P	P	20020530			

US 2002-386816P P 20020607
 US 2002-389123P P 20020613
 US 2002-402207P P 20020809
 US 2002-402407P P 20020809
 US 2002-420860P P 20021024
 US 2003-443062P P 20030128
 US 2003-403676 A2 20030331

L4 ANSWER 2 OF 86 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
 AN 2004:80333 CAPLUS

DN 140:139467

TI Human ***semaphorin*** ***6A*** -like protein (NOV2) and nucleic acid sequences, and their use in antitumor agents and for inhibiting cell migration, angiogenesis, and actin filament formation

IN Alvarez, Enrique; Anderson, David W.; Dhanabal, Mohanraj; Khratsov, Nikolai V.; Laroche, William J.; Lichenstein, Henri S.; Li, Li; Ooi, Chean Eng; Padigaru, Muralidhara; Shimkets, Richard A.; Zhong, Mei

PA USA

SO U.S. Pat. Appl. Publ., 227 pp., Cont.-in-part of Ser. No. US 2003-403676, filed on 31 Mar 2003 which

CODEN: USXXCO

DT Patent

LA English

FAN.CNT 139

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004018977	A1	20040129	US 2003-449548	20030530
	US 6689866	B1	20040210	US 2000-520781	20000308
	US 2004029150	A1	20040212	US 2003-403676	20030331
PRAI	US 1999-123667P	P	19990309		
	US 2000-520781	A2	20000308		
	US 2002-371002P	P	20020409		
	US 2002-384798P	P	20020530		
	US 2002-402407P	P	20020809		
	US 2003-443062P	P	20030128		
	US 2003-403676	A2	20030331		

L4 ANSWER 3 OF 86 USPATFULL on STN

AN 2004:108359 USPATFULL

TI Cell adhesion proteins

IN Duggan, Brendan M., Sunnyvale, CA, UNITED STATES
 Xu, Yuming, Mountain View, CA, UNITED STATES
 Lee, Ernestine A., Castro Valley, CA, UNITED STATES
 Lee, Sally, San Jose, CA, UNITED STATES
 Lu, Dyung Aina M., San Jose, CA, UNITED STATES
 Warren, Bridget A., San Marcos, CA, UNITED STATES
 Yue, Henry, Sunnyvale, CA, UNITED STATES
 Gietzen, Kimberly J., San Jose, CA, UNITED STATES
 Honchell, Cynthia D., San Carlos, CA, UNITED STATES
 Burford, Neil, Durham, CT, UNITED STATES
 Baughn, Mariah R., San Leandro, CA, UNITED STATES
 Tang, Y. Tom, San Jose, CA, UNITED STATES
 Jackson, Jennifer L., Santa Cruz, CA, UNITED STATES
 Gandhi, Ameena R., San Francisco, CA, UNITED STATES
 Kallick, Deborah A., Galveston, TX, UNITED STATES
 Bandman, Olga, Mountain View, CA, UNITED STATES
 Graul, Richard C., San Francisco, CA, UNITED STATES
 Chawla, Narinder K., Union City, CA, UNITED STATES
 Lu, Yan, Mountain View, CA, UNITED STATES
 Ramkumar, Jayalaxmi, Fremont, CA, UNITED STATES
 Yao, Monique G., Mountain View, CA, UNITED STATES
 Lal, Preeti G., Santa Clara, CA, UNITED STATES

PI US 2004082761 A1 20040429
 AI US 2003-451010 A1 20030617 (10)
 WO 2001-US49206 20011218

DT Utility

FS APPLICATION

LN.CNT 6999

INCL INCLM: 530/350.000
 INCLS: 435/006.000; 435/069.100; 435/320.100; 435/325.000; 530/388.220;
 536/023.500; 514/012.000

NCL NCLM: 530/350.000
 NCLS: 435/006.000; 435/069.100; 435/320.100; 435/325.000; 530/388.220;
 536/023.500; 514/012.000

IC [7]

ICM: C12Q001-68

L4 ANSWER 4 OF 86 USPATFULL on STN
 AN 2004:70018 USPATFULL
 TI Novel nucleic acids and polypeptides
 IN Tang, Y. Tom, San Jose, CA, UNITED STATES
 Liu, Chenghua, San Jose, CA, UNITED STATES
 Drmanac, Radoje T., Palo Alto, CA, UNITED STATES
 PI US 2004053245 A1 20040318
 AI US 2003-276774 A1 20030624 (10)
 WO 2001-US3800 20010205
 DT Utility
 FS APPLICATION
 LN.CNT 18750
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000;
 536/023.200; 530/388.100
 NCL NCLM: 435/006.000
 NCLS: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000;
 536/023.200; 530/388.100
 IC [7]
 ICM: C12Q001-68
 ICS: C07H021-04; C12N009-00; C12P021-02; C12N005-06
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 5 OF 86 USPATFULL on STN
 AN 2004:44499 USPATFULL
 TI Proteins and nucleic acids encoding same
 IN Alsobrook, John P., II, Madison, CT, UNITED STATES
 Anderson, David W., Branford, CT, UNITED STATES
 Burgess, Catherine E., Wethersfield, CT, UNITED STATES
 Boldog, Ferenc L., North Haven, CT, UNITED STATES
 Casman, Stacie J., North Haven, CT, UNITED STATES
 Colman, Steven D., Guilford, CT, UNITED STATES
 Edinger, Shlomit R., New Haven, CT, UNITED STATES
 Ellerman, Karen, Branford, CT, UNITED STATES
 Gerlach, Valerie, Branford, CT, UNITED STATES
 Gorman, Linda, Branford, CT, UNITED STATES
 Grosse, William M., Branford, CT, UNITED STATES
 Guo, Xiaojia Sasha, Branford, CT, UNITED STATES
 Herrmann, John L., Guilford, CT, UNITED STATES
 Kekuda, Ramesh, Danbury, CT, UNITED STATES
 Lepley, Denise M., Branford, CT, UNITED STATES
 Li, Li, Branford, CT, UNITED STATES
 MacDougall, John R., Hamden, CT, UNITED STATES
 Millet, Isabelle, Milford, CT, UNITED STATES
 Pena, Carol E. A., New Haven, CT, UNITED STATES
 Peyman, John A., New Haven, CT, UNITED STATES
 Rastelli, Luca, Guilford, CT, UNITED STATES
 Rieger, Daniel K., Branford, CT, UNITED STATES
 Shimkets, Richard A., Guilford, CT, UNITED STATES
 Smithson, Glennda, Guilford, CT, UNITED STATES
 Spytek, Kimberly A., New Haven, CT, UNITED STATES
 Stone, David J., Guilford, CT, UNITED STATES
 Tchernev, Velizar T., Branford, CT, UNITED STATES
 Vernet, Corine A.M., Branford, CT, UNITED STATES
 Voss, Edward Z., Wallingford, CT, UNITED STATES
 Zerhusen, Bryan D., Branford, CT, UNITED STATES
 Zhong, Haihong, Guilford, CT, UNITED STATES
 Zhong, Mei, Branford, CT, UNITED STATES
 PI US 2004033491 A1 20040219
 AI US 2001-16248 A1 20011210 (10)
 PRAI US 2000-254329P 20001208 (60)
 US 2001-291037P 20010515 (60)
 US 2000-255648P 20001214 (60)
 US 2001-297173P 20010608 (60)
 US 2001-309258P 20010731 (60)
 US 2001-326393P 20011001 (60)
 US 2001-315639P 20010829 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 12259
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000;
 536/023.200
 NCL NCLM: 435/006.000

NCLS: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000;
536/023.200

IC [7]

ICM: C12Q001-68

ICS: C07H021-04; C12N009-00; C12P021-02; C12N005-06

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 6 OF 86 USPATFULL on STN

AN 2004:24674 USPATFULL

TI Classification and prognosis prediction of acute lymphoblastic leukemia
by gene expression profiling

IN Downing, James R., Cordova, TN, UNITED STATES

Yeoh, Eng-Juh, Singapore, SINGAPORE

Wilkins, Dawn E., Oxford, MS, UNITED STATES

Wong, Limsoon, Singapore, SINGAPORE

PI US 2004018513 A1 20040129

AI US 2003-391271 A1 20030318 (10)

PRAI US 2002-367144P 20020322 (60)

DT Utility

FS APPLICATION

LN.CNT 9169

INCL INCLM: 435/006.000

NCL NCLM: 435/006.000

IC [7]

ICM: C12Q001-68

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 7 OF 86 USPATFULL on STN

AN 2004:2119 USPATFULL

TI Growth factor homolog ZVEGF4

IN Gilbert, Teresa, Seattle, WA, UNITED STATES

Hart, Charles E., Woodinville, WA, UNITED STATES

Sheppard, Paul O., Granite Falls, WA, UNITED STATES

Gilbertson, Debra G., Seattle, WA, UNITED STATES

PI US 2004002140 A1 20040101

AI US 2001-876813 A1 20010606 (9)

RLI Division of Ser. No. US 2000-564595, filed on 3 May 2000, GRANTED, Pat.

No. US 6495668

PRAI US 1999-132250P 19990503 (60)

US 1999-164463P 19991110 (60)

US 2000-180169P 20000204 (60)

DT Utility

FS APPLICATION

LN.CNT 5092

INCL INCLM: 435/069.400

INCLS: 435/320.100; 435/325.000; 530/399.000; 514/012.000; 536/023.500

NCL NCLM: 435/069.400

NCLS: 435/320.100; 435/325.000; 530/399.000; 514/012.000; 536/023.500

IC [7]

ICM: A61K038-18

ICS: C07K014-475; C07H021-04; C12P021-02; C12N005-06

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 8 OF 86 USPATFULL on STN

AN 2004:34049 USPATFULL

TI Polynucleotides and proteins encoded thereby

IN Shimkets, Richard A., West Haven, CT, United States

PA Curagen Corporation, New Haven, CT, United States (U.S. corporation)

PI US 6689866 B1 20040210

AI US 2000-520781 20000308 (9)

PRAI US 1999-123667P 19990309 (60)

DT Utility

FS GRANTED

LN.CNT 8026

INCL INCLM: 530/350.000

INCLS: 530/350.000; 530/300.000; 435/007.100; 435/006.000; 435/069.100

NCL NCLM: 530/350.000

NCLS: 435/006.000; 435/007.100; 435/069.100; 530/300.000

IC [7]

ICM: C07K001-00

EXF 530/300; 530/350; 435/7.1; 435/6; 435/69.1

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 9 OF 86 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3

AN 2003:972338 CAPLUS

DN 140:35905

TI Semaphorin-like proteins (NOV2) and cDNA sequences and methods of using same for modulating angiogenesis, cell motility, and actin filament formation
 IN Alvarez, Enrique; Anderson, David W.; Dhanabal, Mohanraj; Khramtsov, Nikolai V.; Laroche, William J.; Lichenstein, Henri S.; Li, Li; Ooi, Chean Eng; Padigaru, Muralidhara; Shimkets, Richard A.; Zhong, Mei
 PA Curagen Corporation, USA; Li, Li; et al.
 SO PCT Int. Appl., 197 pp.
 CODEN: PIXXD2

DT Patent
 LA English
 FAN.CNT 139

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003102584	A2	20031211	WO 2003-US17412	20030530
	WO 2003102584	A3	20040219		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
PRAI	US 2004029150	A1	20040212	US 2003-403676	20030331
	US 2002-384798P	P	20020530		
	US 2002-402407P	P	20020809		
	US 2003-443062P	P	20030128		
	US 2003-403676	A2	20030331		
	US 1999-123667P	P	19990309		
US 2000-520781	A2	20000308			

L4 ANSWER 10 OF 86 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
 AN 2003:818529 CAPLUS
 DN 139:318454

TI Human cDNA sequences and their encoded proteins and diagnostic and therapeutic uses
 IN Alsobrook, John P., II; Anderson, David W.; Boldog, Ferenc L.; Burgess, Catherine E.; Casman, Stacie J.; Edinger, Shlomit R.; Gerlach, Valerie L.; Grosse, William M.
 PA Curagen Corporation, USA
 SO PCT Int. Appl., 324 pp.
 CODEN: PIXXD2

DT Patent
 LA English
 FAN.CNT 139

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003085096	A2	20031016	WO 2003-US9929	20030401
		W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
PRAI	US 2003207394	A1	20031106	US 2002-190115	20020703
	US 2004029150	A1	20040212	US 2003-403676	20030331
	US 2002-368996P	P	20020401		
	US 2002-369980P	P	20020404		
	US 2002-370381P	P	20020405		
	US 2002-370969P	P	20020408		
	US 2002-371002P	P	20020409		
	US 2002-372002P	P	20020412		
	US 2002-384297P	P	20020530		
	US 2002-386816P	P	20020607		
US 2002-389123P	P	20020613			
US 2002-402207P	P	20020809			
US 2002-420860P	P	20021024			

US 2003-403676 A2 20030331
US 1999-123667P P 19990309
US 2000-520781 A2 20000308
US 2000-215854P P 20000703
US 2000-215856P P 20000703
US 2000-215902P P 20000703
US 2000-216585P P 20000707
US 2000-216586P P 20000707
US 2000-216722P P 20000707
US 2000-218622P P 20000717
US 2000-218992P P 20000717
US 2000-221285P P 20000727
US 2001-268734P P 20010214
US 2001-274260P P 20010308
US 2001-279856P P 20010329
US 2001-898994 A1 20010703
US 2001-303168P P 20010705

L4 ANSWER 11 OF 86 USPATFULL on STN
AN 2003:330208 USPATFULL
TI Molecules interacting with CASL (MICAL) polynucleotides, polypeptides, and methods of using the same
IN Kolodkin, Alex L., Baltimore, MD, UNITED STATES
Terman, Jon R., Baltimore, MD, UNITED STATES
Mao, Tiany, Parkville, MD, UNITED STATES
Pasterkamp, Ronald J., Baltimore, MD, UNITED STATES
Yu, Hung-Hsiang, Lynnwood, WA, UNITED STATES
PI US 2003232419 A1 20031218
AI US 2003-359012 A1 20030204 (10)
PRAI US 2002-354178P 20020204 (60)
US 2002-384302P 20020530 (60)
US 2002-388325P 20020613 (60)
DT Utility
FS APPLICATION
LN.CNT 10590
INCL INCLM: 435/191.000
INCLS: 435/069.100; 435/320.100; 435/325.000; 530/388.260; 435/006.000;
435/007.200; 536/023.200
NCL NCLM: 435/191.000
NCLS: 435/069.100; 435/320.100; 435/325.000; 530/388.260; 435/006.000;
435/007.200; 536/023.200
IC [7]
ICM: C12Q001-68
ICS: G01N033-53; G01N033-567; C12N009-06; C12P021-02; C12N005-06;
C07K016-40; C07H021-04
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 12 OF 86 USPATFULL on STN
AN 2003:318667 USPATFULL
TI Genes that are up- or down-regulated during differentiation of human embryonic stem cells
IN Stanton, Lawrence W., Singapore, SINGAPORE
Brandenberger, Ralph, Menlo Park, CA, UNITED STATES
Gold, Joseph D., San Francisco, CA, UNITED STATES
Irving, John M., San Mateo, CA, UNITED STATES
Mandalam, Ramkumar, Union City, CA, UNITED STATES
Mok, Michael, Palo Alto, CA, UNITED STATES
Shelton, Dawne, Salt Lake City, UT, UNITED STATES
PI US 2003224411 A1 20031204
AI US 2003-388578 A1 20030313 (10)
DT Utility
FS APPLICATION
LN.CNT 6331
INCL INCLM: 435/006.000
INCLS: 435/007.200; 435/366.000
NCL NCLM: 435/006.000
NCLS: 435/007.200; 435/366.000
IC [7]
ICM: C12Q001-68
ICS: G01N033-53; G01N033-567; C12N005-08
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 13 OF 86 USPATFULL on STN
AN 2003:78594 USPATFULL
TI Novel polynucleotides and proteins encoded thereby
IN Shimkets, Richard A., West Haven, CT, UNITED STATES

PI LaRochelle, William J., Madison, CT, UNITED STATES
US 2003054514 A1 20030320
AI US 2001-957187 A1 20010919 (9)
RLI Continuation of Ser. No. US 2000-520781, filed on 8 Mar 2000, PENDING
PRAI US 1999-123667P 19990309 (60)
US 2000-234082P 20000920 (60)
US 2000-233798P 20000919 (60)
US 2000-174485P 20000104 (60)
DT Utility
FS APPLICATION
LN.CNT 7206
INCL INCLM: 435/183.000
INCLS: 435/069.100; 435/325.000; 435/320.100; 536/023.200
NCL NCLM: 435/183.000
NCLS: 435/069.100; 435/325.000; 435/320.100; 536/023.200
IC [7]
ICM: C12N009-00
ICS: C07H021-04; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 14 OF 86 USPATFULL on STN
AN 2003:3497 USPATFULL
TI Novel nucleic acid sequences encoding human slit-, megf-, and roundabout-like polypeptides
IN Shimkets, Richard A., West Haven, CT, UNITED STATES
PA CuraGen Corporation, New Haven, CT, UNITED STATES, 06511 (U.S. corporation)
PI US 2003003532 A1 20030102
AI US 2001-991053 A1 20011121 (9)
RLI Continuation of Ser. No. US 2000-520781, filed on 8 Mar 2000, PENDING
PRAI WO 2000-US6280 20000309
US 1999-123667P 19990309 (60)
DT Utility
FS APPLICATION
LN.CNT 5323
INCL INCLM: 435/069.100
INCLS: 435/320.100; 435/325.000; 530/350.000; 530/399.000; 536/023.500
NCL NCLM: 435/069.100
NCLS: 435/320.100; 435/325.000; 530/350.000; 530/399.000; 536/023.500
IC [7]
ICM: C07K014-475
ICS: C07H021-04; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 15 OF 86 USPATFULL on STN
AN 2003:279232 USPATFULL
TI Antibodies specific for semaphorin-like polypeptides
IN Boyle, Bryan J., San Francisco, CA, United States
Yeung, George, Mountain View, CA, United States
Arterburn, Matthew C., Los Gatos, CA, United States
Mize, Nancy K., Mountain View, CA, United States
Tang, Y. Tom, San Jose, CA, United States
Liu, Chenghua, San Jose, CA, United States
Drmanac, Radoje T., Palo Alto, CA, United States
PA Nuvelo, Inc., Sunnyvale, CA, United States (U.S. corporation)
PI US 6635742 B1 20031021
AI US 2000-653274 20000831 (9)
RLI Continuation-in-part of Ser. No. US 2000-491404, filed on 25 Jan 2000, now abandoned
DT Utility
FS GRANTED
LN.CNT 5236
INCL INCLM: 530/387.100
INCLS: 435/252.300; 435/320.100; 435/325.000; 435/007.100; 536/023.100;
536/024.100; 424/130.100
NCL NCLM: 530/387.100
NCLS: 424/130.100; 435/007.100; 435/252.300; 435/320.100; 435/325.000;
536/023.100; 536/024.100
IC [7]
ICM: C07K016-00
ICS: G01N033-53; C12N001-20; C12N015-00; C12N015-09; C12N005-00;
C07H021-02; C07H021-04; A61K039-395
EXF 435/7.1; 435/320.1; 435/325; 435/252.3; 536/23.1; 536/24.1; 530/387.1;
424/130.1
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 16 OF 86 USPATFULL on STN
AN 2003:59938 USPATFULL
TI Growth factor homolog zvegf3
IN Gao, Zeren, Redmond, WA, United States
Hart, Charles E., Woodinville, WA, United States
Piddington, Christopher S., Thousand Oaks, CA, United States
Sheppard, Paul O., Granite Falls, WA, United States
Shoemaker, Kimberly E., Bellevue, WA, United States
Gilbertson, Debra G., Seattle, WA, United States
West, James W., Seattle, WA, United States
PA ZymoGenetics, Inc., Seattle, WA, United States (U.S. corporation)
PI US 6528050 B1 20030304
AI US 2000-706968 20001106 (9)
RLI Continuation of Ser. No. US 2000-541752, filed on 31 Mar 2000
Continuation-in-part of Ser. No. US 1999-457066, filed on 7 Dec 1999
PRAI US 1999-165255P 19991112 (60)
US 1999-161653P 19991021 (60)
US 1999-142576P 19990706 (60)
US 1998-111173P 19981207 (60)
DT Utility
FS GRANTED
LN.CNT 4336
INCL INCLM: 424/085.100
INCLS: 424/198.100; 530/351.000; 530/399.000
NCL NCLM: 424/085.100
NCLS: 424/198.100; 530/351.000; 530/399.000
IC [7]
ICM: A61K045-00
EXF 424/85.1; 424/198.1; 530/351; 530/399
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 17 OF 86 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

AN 2004000561 EMBASE
TI Role of semaphorins in the adult nervous system.
AU De Wit J.; Verhaagen J.
CS J. Verhaagen, Graduate School of Neuroscience, Netherlands Inst. for Brain
Research, Meibergdreef 33, 1105 AZ Amsterdam, Netherlands.
j.verhaagen@nih.knaw.nl
SO Progress in Neurobiology, (2003) 71/2-3 (249-267).
Refs: 167
ISSN: 0301-0082 CODEN: PGNBA5
CY United Kingdom
DT Journal; General Review
FS 008 Neurology and Neurosurgery
029 Clinical Biochemistry
LA English
SL English

L4 ANSWER 18 OF 86 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:585151 BIOSIS

DN PREV200300586083
TI SEMA6A, a new molecule for activated langerhans cells.
AU Gautier, G. [Reprint Author]; de Saint-Vis, B. [Reprint Author]; Pin, J.-J. [Reprint Author]; Trinchieri, G. [Reprint Author]; Caux, C. [Reprint Author]; Garrone, P. [Reprint Author]
CS Laboratory for Immunological Research, Schering-Plough, 27, Chemin des Peupliers, 69571, BP11, Dardilly, France
SO European Cytokine Network, (Sept 2003) Vol. 14, No. supplement 3, pp. 94.
print.
Meeting Info.: Annual Meeting of the International Cytokine Society.
Dublin, Ireland. September 20-24, 2003.
ISSN: 1148-5493.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 10 Dec 2003
Last Updated on STN: 10 Dec 2003

L4 ANSWER 19 OF 86 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2004:205153 BIOSIS

DN PREV200400205680
TI Abnormal cerebellar granule cell migration in the cerebellum of
semaphorin ***6A*** - deficient mice.
AU Chedotal, A. [Reprint Author]; Kerjan, G. [Reprint Author]; Cases, o.;
Mitchell, K.

CS CNRS UMR7102, Universite Paris 6, Paris, France
SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2003)
Vol. 2003, pp. Abstract No. 870.5. <http://sfn.scholarone.com>. e-file.
Meeting Info.: 33rd Annual Meeting of the Society of Neuroscience. New
Orleans, LA, USA. November 08-12, 2003. Society of Neuroscience.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 14 Apr 2004
Last Updated on STN: 14 Apr 2004
L4 ANSWER 20 OF 86 USPATFULL on STN
AN 2002:314716 USPATFULL
TI Growth factor homolog zvegf3
IN Gao, Zeren, Redmond, WA, UNITED STATES
Hart, Charles E., Woodinville, WA, UNITED STATES
Piddington, Christopher S., Thousand Oaks, CA, UNITED STATES
Sheppard, Paul O., Granite Falls, WA, UNITED STATES
Shoemaker, Kimberly E., Bellevue, WA, UNITED STATES
Gilbertson, Debra G., Seattle, WA, UNITED STATES
West, James W., Seattle, WA, UNITED STATES
PA ZymoGenetics, Inc. (U.S. corporation)
PI US 2002177193 A1 20021128
AI US 2002-139583 A1 20020502 (10)
RLI Division of Ser. No. US 1999-457066, filed on 7 Dec 1999, PENDING
PRAI US 1998-111173P 19981207 (60)
US 1999-142576P 19990706 (60)
US 1999-161653P 19991021 (60)
US 1999-165255P 19991112 (60)
DT Utility
FS APPLICATION
LN.CNT 5072
INCL INCLM: 435/069.100
INCLS: 435/320.100; 435/325.000; 530/399.000; 536/023.500
NCL NCLM: 435/069.100
NCLS: 435/320.100; 435/325.000; 530/399.000; 536/023.500
IC [7]
ICM: C07K014-475
ICS: C07H021-04; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 21 OF 86 USPATFULL on STN
AN 2002:157101 USPATFULL
TI Snake venom polypeptide zsnk1
IN Sheppard, Paul O., Granite Falls, WA, UNITED STATES
PI US 2002081700 A1 20020627
AI US 2001-923995 A1 20010807 (9)
PRAI US 2000-223164P 20000807 (60)
DT Utility
FS APPLICATION
LN.CNT 3778
INCL INCLM: 435/200.000
INCLS: 435/325.000; 536/023.200; 435/226.000; 435/320.100
NCL NCLM: 435/200.000
NCLS: 435/325.000; 536/023.200; 435/226.000; 435/320.100
IC [7]
ICM: C12N009-24
ICS: C12N009-64; C07H021-04
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 22 OF 86 USPATFULL on STN
AN 2002:332816 USPATFULL
TI Growth factor homolog ZVEGF4
IN Gilbert, Teresa, Seattle, WA, United States
Hart, Charles E., Woodinville, WA, United States
Sheppard, Paul O., Granite Falls, WA, United States
Gilbertson, Debra G., Seattle, WA, United States
PA ZymoGenetics, Inc., Seattle, WA, United States (U.S. corporation)
PI US 6495668 B1 20021217
AI US 2000-564595 20000503 (9)
PRAI US 1999-132250P 19990503 (60)
US 1999-164463P 19991110 (60)
US 2000-180169P 20000204 (60)
DT Utility
FS GRANTED
LN.CNT 4816

INCL INCLM: 530/399.000
INCLS: 435/069.400; 435/070.100; 530/350.000; 536/023.400
NCL NCLM: 530/399.000
NCLS: 435/069.400; 435/070.100; 530/350.000; 536/023.400
IC [7]
ICM: A61K038-24
ICS: A61K038-27; C12N015-09; C07H021-04
EXF 435/69.4; 435/375; 435/377; 514/2; 530/350; 530/402; 530/387.1; 530/399
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 23 OF 86 USPATFULL on STN
AN 2002:201870 USPATFULL
TI Growth factor homolog ZVEGF3
IN Gao, Zeren, Redmond, WA, United States
Hart, Charles E., Woodinville, WA, United States
Piddington, Christopher S., Thousand Oaks, CA, United States
Sheppard, Paul O., Granite Falls, WA, United States
Shoemaker, Kimberly E., Bellevue, WA, United States
Gilbertson, Debra G., Seattle, WA, United States
West, James W., Seattle, WA, United States

PA ZymoGenetics, Inc., Seattle, WA, United States (U.S. corporation)
PI US 6432673 B1 20020813
AI US 1999-457066 19991207 (9)
PRAI US 1998-111173P 19981207 (60)
US 1999-142576P 19990706 (60)
US 1999-161653P 19991021 (60)
US 1999-165255P 19991112 (60)

DT Utility
FS GRANTED

LN.CNT 4888

INCL INCLM: 435/069.100
INCLS: 435/069.500; 435/006.000; 435/320.100; 435/325.000; 530/351.000;
530/399.000

NCL NCLM: 435/069.100
NCLS: 435/006.000; 435/069.500; 435/320.100; 435/325.000; 530/351.000;
530/399.000

IC [7]
ICM: C12N015-00

EXF 435/69.1; 435/69.5; 435/325; 530/351; 530/399

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 24 OF 86 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:139322 BIOSIS
DN PREV200200139322

TI Doing (F/L)PPPPs: EVH1 domains and their proline-rich partners in cell
polarity and migration.

AU Renfranz, Patricia J. [Reprint author]; Beckerle, Mary C. [Reprint author]
CS Department of Biology and Huntsman Cancer Institute, University of Utah,
2000 East Circle of Hope, Salt Lake City, UT, 84112-5550, USA
mary.beckerle@hci.utah.edu

SO Current Opinion in Cell Biology, (February, 2002) vol. 14, No. 1, pp.
88-103. print.

CODEN: COCB3. ISSN: 0955-0674.

DT Article
General Review; (Literature Review)

LA English

ED Entered STN: 6 Feb 2002
Last Updated on STN: 26 Feb 2002

L4 ANSWER 25 OF 86 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2001:545736 CAPLUS

DN 135:148242

TI Human polypeptides and their encoding cDNA sequences and antibodies

IN Ruben, Steven M.; Shi, Yanggu

PA Human Genome Sciences, Inc., USA

SO PCT Int. Appl., 339 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 2001053343	A1	20010726	WO 2001-US1436	20010117
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W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,

LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

EP 1248801 A1 20021016 EP 2001-942641 20010117

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

JP 2003532383 T2 20031105 JP 2001-553815 20010117

PRAI US 2000-176307P P 20000118
WO 2001-US1436 W 20010117

RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 26 OF 86 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 5

AN 2001:169696 BIOSIS

DN PREV200100169696

TI Defining brain wiring patterns and mechanisms through gene trapping in
mice.

AU Leighton, Philip A.; Mitchell, Kevin J.; Goodrich, Lisa V.; Lu, Xiaowei;
Pinson, Kathy; Scherz, Paul; Skarnes, William C.; Tessier-Lavigne, Marc
[Reprint author]

CS Departments of Anatomy and of Biochemistry and Biophysics, Howard Hughes
Medical Institute, University of California, San Francisco, CA,
94143-0452, USA

marctl@itsa.ucsf.edu

SO Nature (London), (8 March, 2001) Vol. 410, No. 6825, pp. 174-179. print.
CODEN: NATUAS. ISSN: 0028-0836.

DT Article

LA English

ED Entered STN: 4 Apr 2001

Last Updated on STN: 18 Feb 2002

L4 ANSWER 27 OF 86 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
2000-10590 BIOTECHDS

TI Nucleic acid coding for human ***semaphorin*** - ***6A*** - ***1***
used as diagnostic agent, therapeutic agent, for modulating immune
system, in gene therapy or for effecting differentiation, cytoskeletal
stabilization and/or plasticity;
plasmid-mediated recombinant protein gene transfer

AU Behl C; Klostermann A

PA Max-Planck-Soc.

LO Munich, Germany.

PI WO 2000031252 2 Jun 2000

AI WO 1999-EP9215 26 Nov 1999

PRAI EP 1998-122441 26 Nov 1998

DT Patent

LA English

OS WPI: 2000-400065 [34]

L4 ANSWER 28 OF 86 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7

AN 2001:61173 BIOSIS

DN PREV200100061173

TI The orthologous human and murine ***semaphorin*** ***6A*** -
1 proteins (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-
stimulated phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
zyxin-like domain.

AU Klostermann, Andreas; Lutz, Beat; Gertler, Frank; Behl, Christian [Reprint
author]

CS Independent Research Group Neurodegeneration, MPI of Psychiatry,
Kraepelinstrasse 2, 80804, Munich, Germany
chris@mpipsykl.mpg.de

SO Journal of Biological Chemistry, (December 15, 2000) Vol. 275, No. 50, pp.
39647-39653. print.

CODEN: JBCHA3. ISSN: 0021-9258.

DT Article

LA English

OS Genbank-AF28866

ED Entered STN: 31 Jan 2001

Last Updated on STN: 15 Feb 2002

L4 ANSWER 29 OF 86 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 8

AN 2000:261050 BIOSIS
DN PREV200000261050
TI The transmembrane protein ***Semaphorin*** ***6A*** repels
embryonic sympathetic axons.
AU Xu, Xiao-Mei; Fisher, Daniel A.; Zhou, Lijuan; White, Fletcher A.; Ng, Sheldon; Snider, William D.; Luo, Yuling [Reprint author]
CS Exelixis Pharmaceuticals, Inc., 260 Littlefield Avenue, South San Francisco, CA, 94080, USA
SO Journal of Neuroscience, (April 1, 2000) Vol. 20, No. 7, pp. 2638-2648.
print.
CODEN: JNRSDS. ISSN: 0270-6474.
DT Article
LA English
ED Entered STN: 21 Jun 2000
Last Updated on STN: 5 Jan 2002

L4 ANSWER 30 OF 86 MEDLINE on STN
AN 1999160821 MEDLINE
DN PubMed ID: 10049528
TI Cloning and characterization of a novel class VI semaphorin, semaphorin Y.
AU Kikuchi K; Chedotal A; Hanafusa H; Ujimasa Y; de Castro F; Goodman C S; Kimura T
CS Sumitomo Pharmaceuticals Research Center, 3-1-98, Kasugade-Naka, Konohana, Osaka, 554-0022, Japan.
SO Molecular and cellular neurosciences, (1999 Jan) 13 (1) 9-23.
Journal code: 9100095. ISSN: 1044-7431.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AB000817; GENBANK-AB013729; GENBANK-AB014074
EM 199904
ED Entered STN: 19990426
Last Updated on STN: 19990426
Entered Medline: 19990415

L4 ANSWER 31 OF 86 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9
AN 1999:59333 BIOSIS
DN PREV199900059333
TI Semaphorins III and IV repel hippocampal axons via two distinct receptors.
AU Chedotal, Alain [Reprint author]; Del Rio, Jose A.; Ruiz, Monica; He, Zhigang; Borrell, Victor; De Castro, Fernando; Ezan, Frederic; Goodman, Corey S.; Tessier-Lavigne, Marc; Sotelo, Constantino; Soriano, Eduardo
CS INSERM U106, Hop. Salpetriere, 75013 Paris, France
SO Development (Cambridge), (Nov., 1998) Vol. 125, No. 21, pp. 4313-4323.
print.
CODEN: DEVPED. ISSN: 0950-1991.
DT Article
LA English
ED Entered STN: 16 Feb 1999
Last Updated on STN: 16 Feb 1999

L4 ANSWER 32 OF 86 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:49302 BIOSIS
DN PREV199900049302
TI Transmembrane protein ***semaphorin*** ***VIA*** is repulsive for
axons of embryonic sympathetic neurons.
AU Xu, X. M. [Reprint author]; Fisher, D. A.; Zhou, L.; Ng, S. [Reprint author]; White, F. A.; Snider, W. D.; Luo, Y. [Reprint author]
CS Exelixis Pharm. Inc., 260 Littlefield Ave., South San Francisco, CA 94080, USA
SO Society for Neuroscience Abstracts, (1998) Vol. 24, No. 1-2, pp. 539.
print.
Meeting Info.: 28th Annual Meeting of the Society for Neuroscience, Part 1. Los Angeles, California, USA. November 7-12, 1998. Society for Neuroscience.
ISSN: 0190-5295.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 10 Feb 1999
Last Updated on STN: 10 Feb 1999

L4 ANSWER 33 OF 86 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 10

AN 1997:373464 CAPLUS
DN 127:106980
TI Cloning and expression of a novel murine semaphorin with structural similarity to insect semaphorin I
AU Zhou, L.; White, F. A.; Lenz, S. I.; Wright, D. E.
CS Center Study Nervous System Injury, Dep. Neurology, Washington Univ., St. Louis, MO, 63110, USA
SO Molecular and Cellular Neuroscience (1997), 9(1), 26-41
CODEN: MOCNED; ISSN: 1044-7431
PB Academic
DT Journal
LA English

L4 ANSWER 34 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAG79413 Protein DGENE
TI New human cell adhesion proteins (CADHP) useful for treating, diagnosing and preventing diseases or conditions associated with the aberrant CADHP expression e.g. cancer, acquired immunodeficiency syndrome, Alzheimer's disease and epilepsy -
IN Duggan B M; Xu Y; Lee E A; Lee S; Lu D A M; Warren B A; Yue H; Gietzen K J; Honchell C D; Burford N; Baughn M R; Tang T Y; Hillman J L; Gandhi A R; Kallick D A; Bandman O; Graul R C; Walia N K; Lu Y; Ramkumar J; Yao M G; Lal P G
PA (INCY-N) INCYTE GENOMICS INC.
PI WO 2002059312 A2 20020801 149p
AI WO 2001-US49206 20011218
PRAI US 2000-256542P 20001218
US 2000-259604P 20001222
US 2001-260101P 20010105
DT Patent
LA English
OS 2002-590826 [63]
CR N-PSDB: ABA00055
DESC CADHP-2, Incyte ID No: 7596315CD1.

L4 ANSWER 35 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN ABB11205 peptide DGENE
TI Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
IN Tang Y T; Liu C; Drmanac R T
PA (HYSE-N) HYSEQ INC.
PI WO 2001057188 A2 20010809 999p
AI WO 2001-US3800 20010205
PRAI US 2000-496914 20000203
US 2000-560875 20000427
DT Patent
LA English
OS 2001-457740 [49]
CR N-PSDB: ABA08449
DESC Human ***semaphorin*** ***via*** homologue, SEQ ID NO:1575.

L4 ANSWER 36 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAB82595 Protein DGENE
TI Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's diseases and cancers -
IN Ruben S M; Shi Y
PA (HUMA-N) HUMAN GENOME SCI INC.
PI WO 2001053343 A1 20010726 339p
AI WO 2001-US1436 20010117
PRAI US 2000-176307 20000118
DT Patent
LA English
OS 2001-483137 [52]
CR N-PSDB: AAH26247
DESC Human secreted protein encoded by cDNA clone HE8QT72.

L4 ANSWER 37 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAY71461 peptide DGENE
TI Nucleic acid coding for human ***semaphorin*** ***6A*** - ***1*** used as diagnostic agent, therapeutic agent, for modulating immune system, in gene therapy or for effecting differentiation, cytoskeletal stabilization and/or plasticity -
IN Behl C; Klostermann A
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI WO 2000031252 A1 20000602 53p
 AI WO 1999-EP9215 19991126
 PRAI EP 1998-122441 19981126
 DT Patent
 LA English
 OS 2000-400065 [34]
 CR N-PSDB: AAD01234
 DESC Binding domain of human ***semaphorin*** ***6A*** - ***1*** .

L4 ANSWER 38 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
 AN AAY71460 Protein DGENE
 TI Nucleic acid coding for human ***semaphorin*** ***6A*** - ***1*** used as diagnostic agent, therapeutic agent, for modulating immune system, in gene therapy or for effecting differentiation, cytoskeletal stabilization and/or plasticity -
 IN Behl C; Klostermann A
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PI WO 2000031252 A1 20000602 53p
 AI WO 1999-EP9215 19991126
 PRAI EP 1998-122441 19981126
 DT Patent
 LA English
 OS 2000-400065 [34]
 CR N-PSDB: AAD01233
 DESC Human ***semaphorin*** ***6A*** - ***1*** .

L4 ANSWER 39 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
 AN ABA00055 cDNA DGENE
 TI New human cell adhesion proteins (CADHP) useful for treating, diagnosing and preventing diseases or conditions associated with the aberrant CADHP expression e.g. cancer, acquired immunodeficiency syndrome, Alzheimer's disease and epilepsy -
 IN Duggan B M; Xu Y; Lee E A; Lee S; Lu D A M; Warren B A; Yue H; Gietzen K J; Honchell C D; Burford N; Baughn M R; Tang T Y; Hillman J L; Gandhi A R; Kallick D A; Bandman O; Graul R C; Walia N K; Lu Y; Ramkumar J; Yao M G; Lal P G
 PA (INCY-N) INCYTE GENOMICS INC.
 PI WO 2002059312 A2 20020801 149p
 AI WO 2001-US49206 20011218
 PRAI US 2000-256542P 20001228
 US 2000-259604P 20001222
 US 2001-260101P 20010105
 DT Patent
 LA English
 OS 2002-590826 [63]
 CR P-PSDB: AAG79413
 DESC CADHP-2 coding sequence, Incyte ID No: 7596315CB1.

L4 ANSWER 40 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
 AN ABA08449 cDNA DGENE
 TI Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
 IN Tang Y T; Liu C; Drmanac R T
 PA (HYSE-N) HYSEQ INC.
 PI WO 2001057188 A2 20010809 999p
 AI WO 2001-US3800 20010205
 PRAI US 2000-496914 20000203
 US 2000-560875 20000427
 DT Patent
 LA English
 OS 2001-457740 [49]
 CR P-PSDB: ABB11205
 DESC Human ***semaphorin*** ***Via*** homologue-encoding cDNA, SEQ ID NO:225.

L4 ANSWER 41 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
 AN AAH26247 cDNA DGENE
 TI Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's diseases and cancers -
 IN Ruben S M; Shi Y
 PA (HUMA-N) HUMAN GENOME SCI INC.
 PI WO 2001053343 A1 20010726 339p
 AI WO 2001-US1436 20010117
 PRAI US 2000-176307 20000118

DT Patent
LA English
OS 2001-483137 [52]
CR P-PSDB: AAB82595
DESC Human secreted protein cDNA clone HE8QT72.

L4 ANSWER 42 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAD01234 DNA DGENE
TI Nucleic acid coding for human ***semaphorin*** ***6A*** - ***1***
used as diagnostic agent, therapeutic agent, for modulating immune
system, in gene therapy or for effecting differentiation, cytoskeletal
stabilization and/or plasticity -
IN Behl C; Klostermann A
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI WO 2000031252 A1 20000602 53p
AI WO 1999-EP9215 19991126
PRAI EP 1998-122441 19981126
DT Patent
LA English
OS 2000-400065 [34]
CR P-PSDB: AAY71461
DESC DNA encoding binding domain of human ***semaphorin*** ***6A*** - ***1*** .

L4 ANSWER 43 OF 86 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAD01233 DNA DGENE
TI Nucleic acid coding for human ***semaphorin*** ***6A*** - ***1***
used as diagnostic agent, therapeutic agent, for modulating immune
system, in gene therapy or for effecting differentiation, cytoskeletal
stabilization and/or plasticity -
IN Behl C; Klostermann A
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI WO 2000031252 A1 20000602 53p
AI WO 1999-EP9215 19991126
PRAI EP 1998-122441 19981126
DT Patent
LA English
OS 2000-400065 [34]
CR P-PSDB: AAY71460
DESC Human ***semaphorin*** ***6A*** - ***1*** CDNA.

L4 ANSWER 44 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): CF132761 GenBank (R)
GenBank ACC. NO. (GBN): CF132761
GenBank VERSION (VER): CF132761.1 GI:40455103
CAS REGISTRY NO. (RN): 634698-57-0
SEQUENCE LENGTH (SQL): 536
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 31 Dec 2003
DEFINITION (DEF): 4-4-A Chick ventral neuroepithelium cDNA library Gallus
gallus cDNA similar to ***Semaphorin*** ***6A***
, mRNA sequence.
KEYWORDS (ST): EST
SOURCE: Gallus gallus (chicken)
ORGANISM (ORGN): Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Archosauria; Aves; Neognathae;
Galliformes; Phasianidae; Phasianinae; Gallus

COMMENT:

Contact: Soula, C.
Centre de Biologie du Developpement, UMR 5547 CNRS/UPS
Universite Paul Sabatier, 118 route de Narbonne, 31062 Toulouse
cedex, France
Tel: 33 5 61 55 64 23
Fax: 33 5 61 55 65 07
Email: soulz@cict.fr
POLYA=No.

REFERENCE: 1 (bases 1 to 536)
AUTHOR (AU): Braquart-Varnier,C.; Clouscard-Martinato,C.; Agius,E.;
Escalas,N.; Danesin,C.; Benazeraf,B.; Cochard,P.;
Soula,C.
TITLE (TI): Identification of new genes expressed in the gliogenic
ventral neuroepithelium
JOURNAL (SO): Unpublished (2003)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..536	/organism="Gallus gallus" / mol-type="mRNA" / db-xref="taxon:9031" / tissue-type="ventral neuroepithelium" / dev-stage="Hamburger Hamilton stage 29-30" / clone-lib="Chick ventral neuroepithelium cDNA library" / note="Vector: pT-Adv; Screening from a subtracted embryonic E6 ventral neuroepithelial cDNA library Chick embryonic ventral neuroepithelial cDNA cloned into pT-Adv using T/A - based cloning system (AdvanTAge PCR cloning kit, Clontech)"

SEQUENCE (SEQ):

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301 cgtggcagta gagaatggga aagaaaaccag aacctcatca atgcctgcac aaaagatatc
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421 attcccagtg tcatggttct gcccattgccc cagcaaggct accaacacgaa gtatgttgac
481 cagccaaaaa tgagcgacgg ggctcagatg tccgtggagg accagaatgc caccct

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L4 ANSWER 45 OF 86

GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BC062979 **GenBank (R)**
GenBank ACC. NO. (GBN): BC062979
GenBank VERSION (VER): BC062979.1 GI:38566245
CAS REGISTRY NO. (RN): 622741-81-5
SEQUENCE LENGTH (SQL): 4139
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Rodents
DATE (DATE): 11 Dec 2003
DEFINITION (DEF): *Mus musculus* sema domain, transmembrane domain (TM), and cytoplasmic domain, (***semaphorin***) ***6A***, mRNA (cDNA clone MGC:86119 IMAGE:6841689), complete cds.

KEYWORDS (ST): MGC
SOURCE: *Mus musculus* (house mouse)
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

COMMENT:

Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.

Web site: <http://genome.uiowa.edu>
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: Plate: Row: Column: 0.

REFERENCE:
AUTHOR (AU):

1 (bases 1 to 4139)
Strausberg,R.L.; Feingold,E.A.; Grouse,L.H.;
Derge,J.G.; Klausner,R.D.; Collins,F.S.; Wagner,L.;
Shenmen,C.M.; Schuler,G.D.; Altschul,S.F.; Zeeberg,B.;
Buetow,K.H.; Schaefer,C.F.; Bhat,N.K.; Hopkins,R.F.;
Jordan,H.; Moore,T.; Max,S.I.; Wang,J.; Hsieh,F.;

Diatchenko, L.; Marusina, K.; Farmer, A.A.; Rubin, G.M.;
 Hong, L.; Stapleton, M.; Soares, M.B.; Bonaldo, M.F.;
 Casavant, T.L.; Scheetz, T.E.; Brownstein, M.J.;
 Usdin, T.B.; Toshiyuki, S.; Carninci, P.; Prange, C.;
 Raha, S.S.; Loquellano, N.A.; Peters, G.J.; Abramson, R.D.;
 Mullahy, S.J.; Bosak, S.A.; McEwan, P.J.; McKernan, K.J.;
 Malek, J.A.; Gunaratne, P.H.; Richards, S.; Worley, K.C.;
 Hale, S.; Garcia, A.M.; Gay, L.J.; Hulyk, S.W.;
 Villalon, D.K.; Muzny, D.M.; Sodergren, E.J.; Lu, X.;
 Gibbs, R.A.; Fahey, J.; Helton, E.; Ketteeman, M.; Madan, A.;
 Rodrigues, S.; Sanchez, A.; Whiting, M.; Madan, A.;
 Young, A.C.; Shevchenko, Y.; Bouffard, G.G.;
 Blakesley, R.W.; Touchman, J.W.; Green, E.D.;
 Dickson, M.C.; Rodriguez, A.C.; Grimwood, J.; Schmutz, J.;
 Myers, R.M.; Butterfield, Y.S.; Krzywinski, M.I.;
 Skalska, U.; Smailus, D.E.; Schnurch, A.; Schein, J.E.;
 Jones, S.J.; Marra, M.A.
TITLE (TI): Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
OTHER SOURCE (OS): CA 138:84323
REFERENCE: 2 (bases 1 to 4139)
AUTHOR (AU): Strausberg, R.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (26-Nov-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4139	/organism="Mus musculus" /mol-type="mRNA" /strain="C57BL/6" /db-xref="taxon:10090" /clone="MGC:86119 IMAGE:6841689" /tissue-type="Brain" /clone-lib="NIH-BMAP-GH0" /lab-host="DH10B" /note="Vector: pYX-ASC" /gene="Sema6a" /note="synonyms: VIa, sema, Sema6A-1, A730020P05Rik" /db-xref="LocusID:20358" /db-xref="MGI:1203727"
gene	1..4139	/codon-start=1 /product="Sema6a protein" /protein-id="AAH62979.1" /db-xref="GI:38566246" /db-xref="LocusID:20358" /translation="MRPAALLLCLTLLCAGAGF PEDSEPISHGNYTKQYPVFVGH KPGRNTTQRHRLDIQMIMMNRTLYVAARDHIYT VDIDTSHTEEIYCSKKLTWKSQRA DVDTCRMKGKHKDECHNFIKVLLKKNDDTLFVCG TNAFNPSCRNYRVDTLETFGDEFS GMARCPYDAKHANIALFADGKLYSATVTDFLAID AVIYRSLGDSPTLRTVKHDSKWLK EPYFVQAVDYGDIYFFFREIAVEYNTMGKVVF RVAQVCKNDMGGSQRVLEKQWTSF LKARLNCSVPGDSHFYFNILQAVTDVIRINGRDV VLATFSTPYNSIPGSAVCAYDMLD IANVFTGRFKEQKSPDSTWTPVPPDERVPKPRPGC CAGSSSLEKYATSNEFPDDTLNFI KTHPLMDEAVPSIINRPWFLRTMVRYRLTKIAVD NAAGPYQNHTVVFLGSEKGIILKF LARIGSSGFLNGSLFLEEMNVYNPEKCSYDGVED KRIMGMQLDRASGSLYVAFSTCVI KVPLGRCERHGKCKKTCIASRDPYCGWVRESGSC AHLSPSLSLRTFEQDIERGNTDGLG DCHNSFVALNGVIRESYLSKNSNDQLVPVTLLAIAV ILAFVMGAVFSGIIVYCVCDHRRK DVAVVQRKEKELTHSRRGSMSSVTKLGLFGDTQ SKDPKPEAILTPLMHNGKLATPSN
CDS	248..3178	

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 SLGPPGTSLSQTGLSKRLEMQHSS
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 /db-xref="CDD:smart00630"
 /note="PSI; Region: domain found
 in Plexins, Semaphorins and
 Integrins"
 /db-xref="CDD:smart00423"

misc-feature 413..1678

misc-feature 1787..1888

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 181 ggccgcctgc ccgtcgatgc accgaaaagg
 241 acctactatg cggccagcag ccttactgt
 301 tggtttccca gaagattccg agccaatcag
 361 tccgggtttt gtggggccaca agccaggacg
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 481 tggatata gacacatccc acacagaaga
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 1201 ttataacagc atcccagggtt ctgcagtctg
 1261 tttcaactggg aggttcaagg aacagaaatc
 1321 cgaacgagtc cctaagccca ggccaggctg
 1381 tgcaaccctcc aatgaggttt ccgtatgatac
 1441 ggacgaggca gtgccttcca tcatcaacag
 1501 ccgcctgacc aaaattgcag tagacaacgc
 1561 tttcctggga tcagaaaagg gaatcatcct
 1621 tttctaaat ggcagcctt tcctggagga
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 1741 actctatgtt gcattctcta cttgtgtat
 1801 tggaaagtgt aaaaaaaacct gcatcgccct
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 1981 gattgggaa agttacctca aaagcaacga
 2041 tgcagtctt cttggctttt tcatggggc
 2101 gtgcgtac cggcgcaaaag acgtggcagt
 2161 ctcgcgtcgg ggtatctatga gcagtgtcac
 2221 gtccaaggac ccaaagccctg aggccatcct
 2281 cacgccttagc aacaccgcca agatgtcat
 2341 cgcctgccc accccagagt ccaccccgac
 2401 cagtgcgcag tgggagagga accagaacat
 2461 catgggttcc cctgtgattc ccacggacct
 2521 cagcgtggtg gtccctggca tcacgcagca
 2581 caaaaatgagc gaggtgggtt ctcagatggc
 2641 taagaccatc aaagagcacc tgatgtacaa
 2701 gaacctggac agcctggccc ctaaaatcc
 2761 aacctcaactg tcacaaaaccc gcctgagca
 2821 tgggtcgaa tataagagga gctacccac
 2881 cactctcaa agaaacaata ctaactctc
 2941 cttggccgg ggagacaacc caccggccgc
 3001 cagctccag ccctctggcc aggccgtgac
 3061 caactcaactg acgagggtcg ggctgaagcg
 3121 caaaccttc tttgcctccc ttccacatc
 3181 ccagggttg gggggccagg agttgaagca
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4081 aatttagttt ctttattttt acaataaatt cactgagtaa ataaaaaaaaa aaaaaaaaaa

L4 ANSWER 46 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BC059238 GenBank (R)
GenBank ACC. NO. (GBN): BC059238
GenBank VERSION (VER): BC059238.1 GI:37748386
CAS REGISTRY NO. (RN): 608850-56-2
SEQUENCE LENGTH (SQL): 4702
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Rodents
DATE (DATE): 20 Oct 2003
DEFINITION (DEF): *Mus musculus* sema domain, transmembrane domain (TM), and cytoplasmic domain, (***semaphorin***) ***6A***, mRNA (cDNA clone MGC:66957 IMAGE:6417475), complete cds.

KEYWORDS (ST): MGC
SOURCE: *Mus musculus* (house mouse)
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathii; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 1255 a 1315 c 1076 g 1056 t

COMMENT:

Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 125 Row: o Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9055333.

REFERENCE: 1 (bases 1 to 4702)
AUTHOR (AU): Strausberg, R.L.; Feingold, E.A.; Grouse, L.H.;
Derge, J.G.; Klausner, R.D.; Collins, F.S.; Wagner, L.;
Shenmen, C.M.; Schuler, G.D.; Altschul, S.F.; Zeeberg, B.;
Buetow, K.H.; Schaefer, C.F.; Bhat, N.K.; Hopkins, R.F.;
Jordan, H.; Moore, T.; Max, S.I.; Wang, J.; Hsieh, F.;
Diatchenko, L.; Marusina, K.; Farmer, A.A.; Rubin, G.M.;
Hong, L.; Stapleton, M.; Soares, M.B.; Bonaldo, M.F.;
Casavant, T.L.; Scheetz, T.E.; Brownstein, M.J.;
Usdin, T.B.; Toshiyuki, S.; Carninci, P.; Prange, C.;
Raha, S.S.; Loquellano, N.A.; Peters, G.J.; Abramson, R.D.;
Mullahy, S.J.; Bosak, S.A.; McEwan, P.J.; McKernan, K.J.;
Malek, J.A.; Gunaratne, P.H.; Richards, S.; Worley, K.C.;
Hale, S.; Garcia, A.M.; Gay, L.J.; Hulyk, S.W.;
Villalon, D.K.; Muzny, D.M.; Sodergren, E.J.; Lu, X.;
Gibbs, R.A.; Fahey, J.; Helton, E.; Ketteman, M.; Madan, A.;
Rodrigues, S.; Sanchez, A.; Whiting, M.; Madan, A.;
Young, A.C.; Shevchenko, Y.; Bouffard, G.G.;
Blakesley, R.W.; Touchman, J.W.; Green, E.D.;
Dickson, M.C.; Rodriguez, A.C.; Grimwood, J.; Schmutz, J.;
Myers, R.M.; Butterfield, Y.S.; Krzywinski, M.I.;
Skalska, U.; Smailus, D.E.; Schnerch, A.; Schein, J.E.;
Jones, S.J.; Marra, M.A.

TITLE (TI): Generation and initial analysis of more than 15,000
full-length human and mouse cDNA sequences

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903
 (2002)
 OTHER SOURCE (OS): CA 138:84323
 REFERENCE:
 AUTHOR (AU): Strausberg, R.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-OCT-2003) National Institutes of Health,
 Mammalian Gene Collection (MGC), Cancer Genomics
 Office, National Cancer Institute, 31 Center Drive,
 Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4702	<code>/organism="Mus musculus"</code> <code>/mol-type="mRNA"</code> <code>/strain="C57BL/6"</code> <code>/db-xref="taxon:10090"</code> <code>/clone="MGC:66957 IMAGE:6417475"</code> <code>/tissue-type="Brain, enriched mouse brain 12.5dpc"</code> <code>/clone-lib="NIH-BMAP-FI0"</code> <code>/lab-host="DH10B"</code> <code>/note="Vector: pYX-ASC"</code> <code>/gene="Sema6a"</code> <code>/note="synonyms: VIa, sema, Sema6A-1, A730020P05Rik"</code> <code>/db-xref="LocusID:20358"</code> <code>/db-xref="MGI:1203727"</code>
gene	1..4702	<code>/codon-start=1</code> <code>/product="Sema6a protein"</code> <code>/protein-id="AAH59238.1"</code> <code>/db-xref="GI:37748387"</code> <code>/db-xref="LocusID:20358"</code> <code>/translation="MRPAALLLC TLLHCAGAGF PEDSEPI SISHGN YTKQYPV FVGH KPGR NTTQRH RL DIQMIM MN R TLYVAARDHI YT VDID TSHTEE IYCSKKL TWKSRQA DVDT CRMKG KHK D ECHNFI K VLLK KND DTLF VCG TNAFNP SCRNY RVD TLETF GDEFS GMARCPY DAKHANIAL FADG KLYS ATV TD FLAID AVIYRSLG DSPTL RTV KHD SKW LK EPYF VQAVD YGDY IYFFF REIA V EYNT MGKV VFP RVAQVCKNDMGG SQRV LEK QWTSF LKARLNCSV PGD SHF YFN ILQAV T DVIR INGR DV VLAT FST PYNSI PG SAV CAY DMLD IANVFTGRF KEQ KSP D STW T PVP D E RVP K P R P G C CAGSSS LEKYAT SNEFP DDT LNF I KTHPLM D E A VPSI I NRPW FL RTM V RY RLT KIA VD NAAGPYQ NH T VVFL GSEK G I I LKF LARI GSSGFL NGS L FLEEM NVY NPEK C SYD GVED K RIM GMQL DRAS G SLY VAF ST C VI KVPLGR CERHG KCKTC IASRD P YCGW VRES GSC AHLSPLS RLT FEQ DIER GNT DGL G DCHNSF VALN GHASS L YP S T T S DAS R D GYES R GGMLD WNDL L EAP GSTD P DPLG AVSS HNHQDKKG VIRESY LK S NDQ L V PVT L AIA VILA FVMGAVFSGI IIVYCV CDH R R K DVA VVQRKE KEL THSRRGSMSSVT KLSGLFGDT QSKD PKPEA ILT P LHMNG KLA TPSNTAK MLIKADQH HLDL TALPT PEST PTLQQKRKP NRGS REWERNQNI I NACT KDMPPM GSPV IPTD LPLR A S P SHIPS VV VLPIT QQGYQ H EY VDQ PKMSEVVAQ M A L E D Q A T L E Y K T I KEHLSSKSPN HGVNL VEN L D S L PPKV P QREAS LG PPGT SLS QTG LSKR LEMQH SSSY G LEYKRSYPT NSL TRSH QTT TLKRN NNTN SSSH L SRNQSFGRGD N P P PAP Q RV D SI QV HSSQPSG QAVTV SRQPSL NAY NSL T R S G L K R T P S L KPDV PPKPSF APLS TSMK PNDAC T" /note="Sema; Region: semaphorin domain" /db-xref="CDD:smart00630" /note="PSI; Region: domain found in Plexins, Semaphorins and Integrins" </code>
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4621 ctggaaataat tgagtttctt tattttaca ataaattcac tgagtaaata atttggagct
4681 ggaaaaaaaaaaaaaa aa

L4 ANSWER 47 OF 86

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LOCUS (LOC): AK082711 GenBank (R)
GenBank ACC. NO. (GBN): AK082711
GenBank VERSION (VER): AK082711.1 GI:26349884
CAS REGISTRY NO. (RN): 485744-81-8
SEQUENCE LENGTH (SQL): 3329
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): High-Throughput CDNA Sequencing
DATE (DATE): 3 Apr 2004
DEFINITION (DEF): Mus musculus 0 day neonate cerebellum cDNA, RIKEN
full-length enriched library, clone:C230094A19
product:sema domain, transmembrane domain (TM), and
cytoplasmic domain, (***semaphorin***) ***6A***
, full insert sequence.
KEYWORDS (ST): HTC; CAP trapper
SOURCE: Mus musculus (house mouse)
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

COMMENT:
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:<http://genome.gsc.riken.jp/>
URL:<http://fantom.gsc.riken.jp/>.

REFERENCE:
1 AUTHOR (AU): Carninci,P.; Hayashizaki,Y.
TITLE (TI): High-efficiency full-length cDNA cloning
JOURNAL (SO): Meth. Enzymol., 303, 19-44 (1999)
OTHER SOURCE (OS): CA 131:318304
REFERENCE:
2 AUTHOR (AU): Carninci,P.; Shibata,Y.; Hayatsu,N.; Sugahara,Y.;
Shibata,K.; Itoh,M.; Konno,H.; Okazaki,Y.;
Muramatsu,M.; Hayashizaki,Y.
TITLE (TI): Normalization and subtraction of cap-trapper-selected
cDNAs to prepare full-length cDNA libraries for rapid
discovery of new genes
JOURNAL (SO): Genome Res., 10 (10), 1617-1630 (2000)
OTHER SOURCE (OS): CA 134:305920
REFERENCE:
3 AUTHOR (AU): Shibata,K.; Itoh,M.; Aizawa,K.; Nagaoka,S.; Sasaki,N.;
Carninci,P.; Konno,H.; Akiyama,J.; Nishi,K.;
Kitsunai,T.; Tashiro,H.; Itoh,M.; Sumi,N.; Ishii,Y.;
Nakamura,S.; Hazama,M.; Nishine,T.; Harada,A.;
Yamamoto,R.; Matsumoto,H.; Sakaguchi,S.; Ikegami,T.;
Kashiwagi,K.; Fujiwaki,S.; Inoue,K.; Togawa,Y.;
Izawa,M.; Ohara,E.; Watahiki,M.; Yoneda,Y.;
Ishikawa,T.; Ozawa,K.; Tanaka,T.; Matsuura,S.;
Kawai,J.; Okazaki,Y.; Muramatsu,M.; Inoue,Y.; Kira,A.;
Hayashizaki,Y.
TITLE (TI): RIKEN integrated sequence analysis (RISA)
JOURNAL (SO): system--384-format sequencing pipeline with 384
REFERENCE:
4 AUTHOR (AU): multicapillary sequencer
TITLE (TI): Genome Res., 10 (11), 1757-1771 (2000)
JOURNAL (SO):
REFERENCE:
5 AUTHOR (AU): The RIKEN Genome Exploration Research Group Phase II
Team; the FANTOM Consortium.
TITLE (TI): Functional annotation of a full-length mouse cDNA
JOURNAL (SO): collection
OTHER SOURCE (OS): Nature, 409, 685-690 (2001)
REFERENCE:
6 AUTHOR (AU): CA 134:203311
TITLE (TI): The FANTOM Consortium; the RIKEN Genome Exploration
JOURNAL (SO): Research Group Phase I & II Team.

TITLE (TI): Analysis of the mouse transcriptome based on functional
 annotation of 60,770 full-length cDNAs
 JOURNAL (SO): Nature, 420, 563-573 (2002)
 OTHER SOURCE (OS): CA 138:131939
 REFERENCE:
 AUTHOR (AU): Adachi,J.; Aizawa,K.; Akimura,T.; Arakawa,T.; Bono,H.; Carninci,P.; Fukuda,S.; Furuno,M.; Hanagaki,T.; Hara,A.; Hashizume,W.; Hayashida,K.; Hayatsu,N.; Hiramoto,K.; Hiraoka,T.; Hirozane,T.; Hori,F.; Imotani,K.; Ishii,Y.; Itoh,M.; Kagawa,I.; Kasukawa,T.; Katoh,H.; Kawai,J.; Kojima,Y.; Kondo,S.; Konno,H.; Kouda,M.; Koya,S.; Kurihara,C.; Matsuyama,T.; Miyazaki,A.; Murata,M.; Nakamura,M.; Nishi,K.; Nomura,K.; Numazaki,R.; Ohno,M.; Ohsato,N.; Okazaki,Y.; Saito,R.; Saitoh,H.; Sakai,C.; Sakai,K.; Sakazume,N.; Sano,H.; Sasaki,D.; Shibata,K.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Tagami,M.; Tagawa,A.; Takahashi,F.; Takaku-Akahira,S.; Takeda,Y.; Tanaka,T.; Tomaru,A.; Toya,T.; Yasunishi,A.; Muramatsu,M.; Hayashizaki,Y.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)

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L4 ANSWER 48 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

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GenBank VERSION (VER): AK052232.1 GI:26342457
CAS REGISTRY NO. (RN): 492936-40-0
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MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): High-Throughput CDNA Sequencing
DATE (DATE): 3 Apr 2004
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full insert sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

COMMENT:

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.
URL:<http://genome.gsc.riken.jp/>
URL:<http://fantom.gsc.riken.jp/>.

REFERENCE:

1

AUTHOR (AU): Carninci,P.; Hayashizaki,Y.
TITLE (TI): High-efficiency full-length cDNA cloning
JOURNAL (SO): Meth. Enzymol., 303, 19-44 (1999)
OTHER SOURCE (OS): CA 131:318304

2

AUTHOR (AU): Carninci,P.; Shibata,Y.; Hayatsu,N.; Sugahara,Y.;
Shibata,K.; Itoh,M.; Konno,H.; Okazaki,Y.;
Muramatsu,M.; Hayashizaki,Y.
TITLE (TI): Normalization and subtraction of cap-trapper-selected
cDNAs to prepare full-length cDNA libraries for rapid
discovery of new genes
JOURNAL (SO): Genome Res., 10 (10), 1617-1630 (2000)
OTHER SOURCE (OS): CA 134:305920

3

AUTHOR (AU): Shibata,K.; Itoh,M.; Aizawa,K.; Nagaoka,S.; Sasaki,N.;
Carninci,P.; Konno,H.; Akiyama,J.; Nishi,K.;
Kitsunai,T.; Tashiro,H.; Itoh,M.; Sumi,N.; Ishii,Y.;
Nakamura,S.; Hazama,M.; Nishine,T.; Harada,A.;
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Kashiwagi,K.; Fujiwake,S.; Inoue,K.; Togawa,Y.;
Izawa,M.; Ohara,E.; Watahiki,M.; Yoneda,Y.;
Ishikawa,T.; Ozawa,K.; Tanaka,T.; Matsuura,S.;
Kawai,J.; Okazaki,Y.; Muramatsu,M.; Inoue,Y.; Kira,A.;
Hayashizaki,Y.

TITLE (TI): RIKEN integrated sequence analysis (RISA)
system--384-format sequencing pipeline with 384
multicapillary sequencer

4

AUTHOR (AU): The RIKEN Genome Exploration Research Group Phase II
Team; the FANTOM Consortium.

TITLE (TI): Functional annotation of a full-length mouse cDNA
collection

JOURNAL (SO): Nature, 409, 685-690 (2001)
OTHER SOURCE (OS): CA 134:203311

5

AUTHOR (AU): The FANTOM Consortium; the RIKEN Genome Exploration
Research Group Phase I & II Team.
TITLE (TI): Analysis of the mouse transcriptome based on functional
annotation of 60,770 full-length cDNAs

JOURNAL (SO): Nature, 420, 563-573 (2002)
OTHER SOURCE (OS): CA 138:131939

6 (bases 1 to 4476)

AUTHOR (AU): Adachi,J.; Aizawa,K.; Akimura,T.; Arakawa,T.; Bono,H.;
Carninci,P.; Fukuda,S.; Furuno,M.; Hanagaki,T.;
Hara,A.; Hashizume,W.; Hayashida,K.; Hayatsu,N.;
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Takahashi,F.; Takaku-Akahira,S.; Takeda,Y.; Tanaka,T.;
Tomaru,A.; Toya,T.; Yasunishi,A.; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (16-JUL-2001) Yoshihide Hayashizaki, The
Institute of Physical and Chemical Research (RIKEN),
Laboratory for Genome Exploration Research Group, RIKEN
Genomic Sciences Center (GSC), RIKEN Yokohama

Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-
 res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>,
 Tel:81-45-503-9222, Fax:81-45-503-9216)

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LOCUS (LOC): AK042751 GenBank (R)
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GenBank VERSION (VER): AK042751.1 GI:26335300
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DIVISION CODE (CI): High-Throughput CDNA Sequencing
DATE (DATE): 3 Apr 2004
DEFINITION (DEF): Mus musculus 7 days neonate cerebellum cDNA, RIKEN
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product:sema domain, transmembrane domain (TM), and
cytoplasmic domain, (***semaphorin***) ***6A***
, full insert sequence.
KEYWORDS (ST): HTC; CAP trapper
SOURCE: Mus musculus (house mouse)
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
COMMENT:
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL:<http://genome.gsc.riken.jp/>

URL:<http://fantom.gsc.riken.jp/>.

REFERENCE: 1
AUTHOR (AU): Carninci,P.; Hayashizaki,Y.
TITLE (TI): High-efficiency full-length cDNA cloning
JOURNAL (SO): Meth. Enzymol., 303, 19-44 (1999)
OTHER SOURCE (OS): CA 131:318304

REFERENCE: 2
AUTHOR (AU): Carninci,P.; Shibata,Y.; Hayatsu,N.; Sugahara,Y.;
Shibata,K.; Itoh,M.; Konno,H.; Okazaki,Y.;
Muramatsu,M.; Hayashizaki,Y.
TITLE (TI): Normalization and subtraction of cap-trapper-selected
cDNAs to prepare full-length cDNA libraries for rapid
discovery of new genes
JOURNAL (SO): Genome Res., 10 (10), 1617-1630 (2000)
OTHER SOURCE (OS): CA 134:305920

REFERENCE: 3
AUTHOR (AU): Shibata,K.; Itoh,M.; Aizawa,K.; Nagaoka,S.; Sasaki,N.;
Carninci,P.; Konno,H.; Akiyama,J.; Nishi,K.;
Kitsunai,T.; Tashiro,H.; Itoh,M.; Sumi,N.; Ishii,Y.;
Nakamura,S.; Hazama,M.; Nishine,T.; Harada,A.;
Yamamoto,R.; Matsumoto,H.; Sakaguchi,S.; Ikegami,T.;
Kashiwagi,K.; Fujiwake,S.; Inoue,K.; Togawa,Y.;
Izawa,M.; Ohara,E.; Watahiki,M.; Yoneda,Y.;
Ishikawa,T.; Ozawa,K.; Tanaka,T.; Matsuura,S.;
Kawai,J.; Okazaki,Y.; Muramatsu,M.; Inoue,Y.; Kira,A.;
Hayashizaki,Y.
TITLE (TI): RIKEN integrated sequence analysis (RISA)
system--384-format sequencing pipeline with 384
multicapillary sequencer
JOURNAL (SO): Genome Res., 10 (11), 1757-1771 (2000)

REFERENCE: 4
AUTHOR (AU): The RIKEN Genome Exploration Research Group Phase II
Team; the FANTOM Consortium.
TITLE (TI): Functional annotation of a full-length mouse cDNA
collection
JOURNAL (SO): Nature, 409, 685-690 (2001)
OTHER SOURCE (OS): CA 134:203311

REFERENCE: 5
AUTHOR (AU): The FANTOM Consortium; the RIKEN Genome Exploration
Research Group Phase I & II Team.
TITLE (TI): Analysis of the mouse transcriptome based on functional
annotation of 60,770 full-length cDNAs
JOURNAL (SO): Nature, 420, 563-573 (2002)
OTHER SOURCE (OS): CA 138:131939

REFERENCE: 6 (bases 1 to 3226)
AUTHOR (AU): Adachi,J.; Aizawa,K.; Akimura,T.; Arakawa,T.; Bono,H.;
Carninci,P.; Fukuda,S.; Furuno,M.; Hanagaki,T.;
Hara,A.; Hashizume,W.; Hayashida,K.; Hayatsu,N.;
Hiramoto,K.; Hiraoka,T.; Hirozane,T.; Hori,F.;
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Katoh,H.; Kawai,J.; Kojima,Y.; Kondo,S.; Konno,H.;
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Nomura,K.; Numazaki,R.; Ohno,M.; Ohsato,N.; Okazaki,Y.;
Saito,R.; Saitoh,H.; Sakai,C.; Sakai,K.; Sakazume,N.;
Sano,H.; Sasaki,D.; Shibata,K.; Shinagawa,A.;
Shiraki,T.; Sogabe,Y.; Tagami,M.; Tagawa,A.;
Takahashi,F.; Takaku-Akahira,S.; Takeda,Y.; Tanaka,T.;
Tomaru,A.; Toya,T.; Yasunishi,A.; Muramatsu,M.;
Hayashizaki,Y.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (16-JUL-2001) Yoshihide Hayashizaki, The
Institute of Physical and Chemical Research (RIKEN),
Laboratory for Genome Exploration Research Group, RIKEN
Genomic Sciences Center (GSC), RIKEN Yokohama
Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-
res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>,
Tel:81-45-503-9222, Fax:81-45-503-9216)

FEATURES (FEAT):

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L4 ANSWER 50 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AK084922 GenBank (R)
GenBank ACC. NO. (GBN): AK084922
GenBank VERSION (VER): AK084922.1 GI:26102335
CAS REGISTRY NO. (RN): 492839-41-5
SEQUENCE LENGTH (SQL): 3921
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): High-Throughput CDNA Sequencing
DATE (DATE): 3 Apr 2004
DEFINITION (DEF): *Mus musculus* 13 days embryo lung cDNA, RIKEN
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product:weakly similar to ***SEMAPHORIN***
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full insert sequence.

KEYWORDS (ST): HTC; CAP trapper
SOURCE: *Mus musculus* (house mouse)
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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Sciurognathi; Muridae; Murinae; *Mus*

COMMENT:
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:<http://genome.gsc.riken.jp/>
URL:<http://fantom.gsc.riken.jp/>.

REFERENCE: 1
AUTHOR (AU): Carninci, P.; Hayashizaki, Y.
TITLE (TI): High-efficiency full-length cDNA cloning
JOURNAL (SO): Meth. Enzymol., 303, 19-44 (1999)
OTHER SOURCE (OS): CA 131:318304
REFERENCE: 2
AUTHOR (AU): Carninci, P.; Shibata, Y.; Hayatsu, N.; Sugahara, Y.;
Shibata, K.; Itoh, M.; Konno, H.; Okazaki, Y.;
Muramatsu, M.; Hayashizaki, Y.
TITLE (TI): Normalization and subtraction of cap-trapper-selected
cDNAs to prepare full-length cDNA libraries for rapid
discovery of new genes
JOURNAL (SO): Genome Res., 10 (10), 1617-1630 (2000)
OTHER SOURCE (OS): CA 134:305920
REFERENCE: 3
AUTHOR (AU): Shibata, K.; Itoh, M.; Aizawa, K.; Nagaoka, S.; Sasaki, N.;
Carninci, P.; Konno, H.; Akiyama, J.; Nishi, K.;
Kitsunai, T.; Tashiro, H.; Itoh, M.; Sumi, N.; Ishii, Y.;
Nakamura, S.; Hazama, M.; Nishine, T.; Harada, A.;
Yamamoto, R.; Matsumoto, H.; Sakaguchi, S.; Ikegami, T. ;

Kashiwagi, K.; Fujiwake, S.; Inoue, K.; Togawa, Y.;
 Izawa, M.; Ohara, E.; Watahiki, M.; Yoneda, Y.;
 Ishikawa, T.; Ozawa, K.; Tanaka, T.; Matsuura, S.;
 Kawai, J.; Okazaki, Y.; Muramatsu, M.; Inoue, Y.; Kira, A.;
 Hayashizaki, Y.
TITLE (TI): RIKEN integrated sequence analysis (RISA)
JOURNAL (SO): system--384-format sequencing pipeline with 384
REFERENCE: multicapillary sequencer
AUTHOR (AU): Genome Res., 10 (11), 1757-1771 (2000)
TITLE (TI): 4
JOURNAL (SO): The RIKEN Genome Exploration Research Group Phase II
REFERENCE: AUTHOR (AU): Team; the FANTOM Consortium.
TITLE (TI): Functional annotation of a full-length mouse cDNA
JOURNAL (SO): collection
OTHER SOURCE (OS): Nature, 409, 685-690 (2001)
REFERENCE: CA 134:203311
AUTHOR (AU): 5
TITLE (TI): The FANTOM Consortium; the RIKEN Genome Exploration
REFERENCE: Research Group Phase I & II Team.
JOURNAL (SO): Analysis of the mouse transcriptome based on functional
OTHER SOURCE (OS): annotation of 60,770 full-length cDNAs
REFERENCE: CA 138:131939
AUTHOR (AU): 6 (bases 1 to 3921)
TITLE (TI): Adachi, J.; Aizawa, K.; Akimura, T.; Arakawa, T.; Bono, H.;
JOURNAL (SO): Carninci, P.; Fukuda, S.; Furuno, M.; Hanagaki, T.;
 Hara, A.; Hashizume, W.; Hayashida, K.; Hayatsu, N.;
 Hiramoto, K.; Hiraoka, T.; Hirozane, T.; Hori, F.;
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 Miyazaki, A.; Murata, M.; Nakamura, M.; Nishi, K.;
 Nomura, K.; Numazaki, R.; Ohno, M.; Ohsato, N.; Okazaki, Y.;
 Saito, R.; Saitoh, H.; Sakai, C.; Sakai, K.; Sakazume, N.;
 Sano, H.; Sasaki, D.; Shibata, K.; Shinagawa, A.;
 Shiraki, T.; Sogabe, Y.; Tagami, M.; Tagawa, A.;
 Takahashi, F.; Takaku-Akahira, S.; Takeda, Y.; Tanaka, T.;
 Tomaru, A.; Toya, T.; Yasunishi, A.; Muramatsu, M.;
 Hayashizaki, Y.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (16-APR-2002) Yoshihide Hayashizaki, The
 Institute of Physical and Chemical Research (RIKEN),
 Laboratory for Genome Exploration Research Group, RIKEN
 Genomic Sciences Center (GSC), RIKEN Yokohama
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 Kanagawa 230-0045, Japan (E-mail: genome-
 res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>,
 Tel: 81-45-503-9222, Fax: 81-45-503-9216)

FEATURES (FEAT):

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 3901 tagattttac acctctcttgc

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LOCUS (LOC): AK084029 GenBank (R)
 GenBank ACC. NO. (GBN): AK084029
 GenBank VERSION (VER): AK084029.1 GI:26101651
 CAS REGISTRY NO. (RN): 492832-57-2
 SEQUENCE LENGTH (SQL): 3105
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): High-Throughput CDNA Sequencing
 DATE (DATE): 3 Apr 2004
 DEFINITION (DEF): Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN
 full-length enriched library, clone:D130077F24
 product:weakly similar to ***SEMAPHORIN***
 6A PRECURSOR (***SEMAPHORIN***) ***VIA***

) (SEMA VIA) (SEMAPHORIN Q) (SEMA Q) [Mus musculus],
full insert sequence.

KEYWORDS (ST): HTC; CAP trapper

SOURCE: Mus musculus (house mouse)

ORGANISM (ORGN): Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

COMMENT:

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:<http://genome.gsc.riken.jp/>

URL:<http://fantom.gsc.riken.jp/>

REFERENCE: 1

AUTHOR (AU): Carninci,P.; Hayashizaki,Y.
TITLE (TI): High-efficiency full-length cDNA cloning
JOURNAL (SO): Meth. Enzymol., 303, 19-44 (1999)
OTHER SOURCE (OS): CA 131:318304

REFERENCE: 2

AUTHOR (AU): Carninci,P.; Shibata,Y.; Hayatsu,N.; Sugahara,Y.;
Shibata,K.; Itoh,M.; Konno,H.; Okazaki,Y.;
Muramatsu,M.; Hayashizaki,Y.
TITLE (TI): Normalization and subtraction of cap-trapper-selected
JOURNAL (SO): Genomes to prepare full-length cDNA libraries for rapid
OTHER SOURCE (OS): CA 134:305920
discovery of new genes

REFERENCE: 3

AUTHOR (AU): Shibata,K.; Itoh,M.; Aizawa,K.; Nagaoka,S.; Sasaki,N.;
Carninci,P.; Konno,H.; Akiyama,J.; Nishi,K.;
Kitsunai,T.; Tashiro,H.; Itoh,M.; Sumi,N.; Ishii,Y.;
Nakamura,S.; Hazama,M.; Nishine,T.; Harada,A.;
Yamamoto,R.; Matsumoto,H.; Sakaguchi,S.; Ikegami,T.;
Kashiwagi,K.; Fujiwaki,S.; Inoue,K.; Togawa,Y.;
Izawa,M.; Ohara,E.; Watahiki,M.; Yoneda,Y.;
Ishikawa,T.; Ozawa,K.; Tanaka,T.; Matsuura,S.;
Kawai,J.; Okazaki,Y.; Muramatsu,M.; Inoue,Y.; Kira,A.;
Hayashizaki,Y.

TITLE (TI): RIKEN integrated sequence analysis (RISA)
JOURNAL (SO): system--384-format sequencing pipeline with 384
multicapillary sequencer

REFERENCE: 4

AUTHOR (AU): The RIKEN Genome Exploration Research Group Phase II
Team; the FANTOM Consortium.
TITLE (TI): Functional annotation of a full-length mouse cDNA
JOURNAL (SO): collection
OTHER SOURCE (OS): Nature, 409, 685-690 (2001)
CA 134:203311

REFERENCE: 5

AUTHOR (AU): The FANTOM Consortium; the RIKEN Genome Exploration
Research Group Phase I & II Team.
TITLE (TI): Analysis of the mouse transcriptome based on functional
JOURNAL (SO): annotation of 60,770 full-length cDNAs
OTHER SOURCE (OS): Nature, 420, 563-573 (2002)
CA 138:131939

REFERENCE: 6 (bases 1 to 3105)

AUTHOR (AU): Adachi,J.; Aizawa,K.; Akimura,T.; Arakawa,T.; Bono,H.;
Carninci,P.; Fukuda,S.; Furuno,M.; Hanagaki,T.;
Hara,A.; Hashizume,W.; Hayashida,K.; Hayatsu,N.;
Hiramoto,K.; Hiraoka,T.; Hirozane,T.; Hori,F.;
Imotani,K.; Ishii,Y.; Itoh,M.; Kagawa,I.; Kasukawa,T.;
Katoh,H.; Kawai,J.; Kojima,Y.; Kondo,S.; Konno,H.;
Kouda,M.; Koya,S.; Kurihara,C.; Matsuyama,T.;
Miyazaki,A.; Murata,M.; Nakamura,M.; Nishi,K.;
Nomura,K.; Numazaki,R.; Ohno,M.; Ohsato,N.; Okazaki,Y.;
Saito,R.; Saitoh,H.; Sakai,C.; Sakai,K.; Sakazume,N.;
Sano,H.; Sasaki,D.; Shibata,K.; Shinagawa,A.;
Shiraki,T.; Sogabe,Y.; Tagami,M.; Tagawa,A.;
Takahashi,F.; Takaku-Akahira,S.; Takeda,Y.; Tanaka,T.;
Tomaru,A.; Toya,T.; Yasunishi,A.; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (16-APR-2002) Yoshihide Hayashizaki, The
 Institute of Physical and Chemical Research (RIKEN),
 Laboratory for Genome Exploration Research Group, RIKEN
 Genomic Sciences Center (GSC), RIKEN Yokohama
 Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-
 res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>,
 Tel:81-45-503-9222, Fax:81-45-503-9216)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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misc-feature	<1..646	
polyA-signal	3086..3091	/note="putative"
polyA-site	3105	/note="putative"

SEQUENCE (SEQ):

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 121 gatccatatg gctcatcaaa ccctcatgtc ggaccgggt ggaccaatgg ctgaggccc
 181 acccaaggc cctaaccggt aggcatctct atactccctt ccctccacac tccccagaaa
 241 tagtccaacc aagagagtag atgtccccac cactcctggg gtgccaatga cttctctgga
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 361 aaaccttaaac tcaccaaatagt gtgtttgtt atctagacag ccgagtatga accgtggagg
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 481 tcatctgcag ccctccctt ccagacagag cagctatacc agtaatggca ccctccccag
 541 gacgggacta aagaggacac catccttaaa acctgtatgt ccaccaaaggc cttcctttgt
 601 tccgc当地 accatctgtca gaccactgaa caagtacacg tactaggct caagtatgt
 661 attccctgtt ggctttatcc tgccctgtc gttgcagga agctgtgagg gtaccttcag
 721 atgagatacc tgcttgattt ttaagagaaa caagtagcca aaaaactct gtcactttgg
 781 taacaccaga acttgccaca ttagtactt acagcaaggc ttctgtgtac ttgcccggaaa
 841 cgaaggggagg tcctgctcac tccatttctt tcggttgaag cagaaggat gtgttagccag
 901 ggaaggctcc cttcaccagt gtaaaagagct gatacgtac tcagaagact gaacaaatac
 961 ttgaaaatgg gttcaatgtt gactgcccatt ctgtgtgtc ttcccattaa atgtgaacat
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 1681 tcaacccctttag acacacttac aggcttttat tttgattgtt ttattttattt ttccatata
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 1921 tttgctcatg agtcatgtc gcaatgtt gtaactgtt ataccatgt tgatgttacc
 1981 tggatctgtg cattttgtc cttatttactt cggatgtt gatgttccgcg gtatgttgg
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 2101 ctgaggactt cttatacgt cataaaagcca ccttagagcgta ttgttgggtt agcaacgcgg
 2161 cccctccctt ccaggatcatc aagcagcacc cacccttgcg atgataaaca ttccatcccc
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 2281 ccatgtctag agtcgtttt atgttagctt gcaagaccca ctgtatggctt caggtgtgt
 2341 gcctactgac agcttgggtt aaccactgc acatcacca gtcatttacc caacttactc
 2401 tagaaatgtt cacagctaa gaaaggctt gacccatgtca ggcggagttc aagtgtatc
 2461 ttggacagt gaccatgtt gtcatttactt gggggaggat ggggtacaag acaccagatc

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2581 tctatagaaa aatgattccc tgtgatctt tggaagctcc aaagctaaa cccttcagct
2641 ttgcaactaa aaatattaca gtttataat caattaaacc aacaacaat aagcactaca
2701 catctgccac caacaatgtt gtttgcattt accttacca tattaatccc agcgtggtaa
2761 ctctgtgtga ccccgataac atttgttaac attgtgcgtc ctttagagttt gtactgttag
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3001 aacgtgtata gatatcttgt aaacttgtat tgtggatgtg taaaataat gtactttggg
3061 ttttaaacac cgcatgtaaa gtcacaaataa aatatccaag tcatt

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LOCUS (LOC): AK078490 GenBank (R)
GenBank ACC. NO. (GBN): AK078490
GenBank VERSION (VER): AK078490.1 GI:26097898
CAS REGISTRY NO. (RN): 492822-90-9
SEQUENCE LENGTH (SQL): 3509
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): High-Throughput CDNA Sequencing
DATE (DATE): 3 Apr 2004
DEFINITION (DEF): *Mus musculus* 12 days embryo female mullerian duct
includes surrounding region cDNA, RIKEN full-length
enriched library, clone:6820415J05 product:sema domain,
transmembrane domain (TM), and cytoplasmic domain, (***semaphorin***) ***6A*** , full insert sequence.

KEYWORDS (ST): HTC; CAP trapper
SOURCE: *Mus musculus* (house mouse)
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

COMMENT:
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:<http://genome.gsc.riken.jp/>
URL:<http://fantom.gsc.riken.jp/>.

REFERENCE:
1
AUTHOR (AU): Carninci,P.; Hayashizaki,Y.
TITLE (TI): High-efficiency full-length cDNA cloning
JOURNAL (SO): Meth. Enzymol., 303, 19-44 (1999)
OTHER SOURCE (OS): CA 131:318304
REFERENCE:
2
AUTHOR (AU): Carninci,P.; Shibata,Y.; Hayatsu,N.; Sugahara,Y.;
Shibata,K.; Itoh,M.; Konno,H.; Okazaki,Y.;
Muramatsu,M.; Hayashizaki,Y.
TITLE (TI): Normalization and subtraction of cap-trapper-selected
cDNAs to prepare full-length cDNA libraries for rapid
discovery of new genes
JOURNAL (SO): Genome Res., 10 (10), 1617-1630 (2000)
OTHER SOURCE (OS): CA 134:305920
REFERENCE:
3
AUTHOR (AU): Shibata,K.; Itoh,M.; Aizawa,K.; Nagaoka,S.; Sasaki,N.;
Carninci,P.; Konno,H.; Akiyama,J.; Nishi,K.;
Kitsunai,T.; Tashiro,H.; Itoh,M.; Sumi,N.; Ishii,Y.;
Nakamura,S.; Hazama,M.; Nishine,T.; Harada,A.;
Yamamoto,R.; Matsumoto,H.; Sakaguchi,S.; Ikegami,T.;
Kashiwagi,K.; Fujiwaki,S.; Inoue,K.; Togawa,Y.;
Izawa,M.; Ohara,E.; Watahiki,M.; Yoneda,Y.;
Ishikawa,T.; Ozawa,K.; Tanaka,T.; Matsuura,S.;
Kawai,J.; Okazaki,Y.; Muramatsu,M.; Inoue,Y.; Kira,A.;
Hayashizaki,Y.
TITLE (TI): RIKEN integrated sequence analysis (RISA)
system--384-format sequencing pipeline with 384
multicapillary sequencer
JOURNAL (SO): Genome Res., 10 (11), 1757-1771 (2000)
REFERENCE:
4
AUTHOR (AU): The RIKEN Genome Exploration Research Group Phase II
Team; the FANTOM Consortium.
TITLE (TI): Functional annotation of a full-length mouse cDNA
collection
JOURNAL (SO): Nature, 409, 685-690 (2001)

OTHER SOURCE (OS): CA 134:203311
REFERENCE:
AUTHOR (AU): The FANTOM Consortium; the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE (TI): Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL (SO): Nature, 420, 563-573 (2002)
OTHER SOURCE (OS): CA 138:131939
REFERENCE:
AUTHOR (AU): 6 (bases 1 to 3509)
Adachi,J.; Aizawa,K.; Akimura,T.; Arakawa,T.; Bono,H.; Carninci,P.; Fukuda,S.; Furuno,M.; Hanagaki,T.; Hara,A.; Hashizume,W.; Hayashida,K.; Hayatsu,N.; Hiramoto,K.; Hiraoka,T.; Hirozane,T.; Hori,F.; Imotani,K.; Ishii,Y.; Itoh,M.; Kagawa,I.; Kasukawa,T.; Katoh,H.; Kawai,J.; Kojima,Y.; Kondo,S.; Konno,H.; Kouda,M.; Koya,S.; Kurihara,C.; Matsuyama,T.; Miyazaki,A.; Murata,M.; Nakamura,M.; Nishi,K.; Nomura,K.; Numazaki,R.; Ohno,M.; Ohsato,N.; Okazaki,Y.; Saito,R.; Saitoh,H.; Sakai,C.; Sakai,K.; Sakazume,N.; Sano,H.; Sasaki,D.; Shibata,K.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Tagami,M.; Tagawa,A.; Takahashi,F.; Takaku-Akahira,S.; Takeda,Y.; Tanaka,T.; Tomaru,A.; Toya,T.; Yasunishi,A.; Muramatsu,M.; Hayashizaki,Y.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)

FEATURES (FEAT):			
Feature Key	Location	Qualifier	
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3361 agcctttcc tggaggagat gaatgtttac aaccggaaa agtgagtgaa acgttgggt
3421 ctttcttgc aactattgttattactgc tggtatcaca ccgtttccgc
3481 agacaagtttgc

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LOCUS (LOC): AK031307 GenBank (R)
GenBank ACC. NO. (GBN): AK031307
GenBank VERSION (VER): AK031307.1 GI:26082260
CAS REGISTRY NO. (RN): 486370-53-0
SEQUENCE LENGTH (SQL): 4374
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): High-Throughput cDNA Sequencing
DATE (DATE): 3 Apr 2004
DEFINITION (DEF): *Mus musculus* 13 days embryo male testis cDNA, RIKEN
full-length enriched library, clone:6030405B10
product:weakly similar to ***SEMAPHORIN***
 6A PRECURSOR (***SEMAPHORIN*** ***VIA***
) (SEMA VIA) (SEMAPHORIN Q) (SEMA Q) [Mus musculus],
full insert sequence.
KEYWORDS (ST): HTC; CAP trapper
SOURCE: *Mus musculus* (house mouse)
ORGANISM (ORGN): *Mus musculus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; *Mus*

COMMENT: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL:<http://genome.gsc.riken.jp/>
URL:<http://fantom.gsc.riken.jp/>.

OTHER SOURCE (OS): CA 131:318304
 REFERENCE: 2
 AUTHOR (AU): Carninci,P.; Shibata,Y.; Hayatsu,N.; Sugahara,Y.;
 Shibata,K.; Itoh,M.; Konno,H.; Okazaki,Y.;
 Muramatsu,M.; Hayashizaki,Y.
 TITLE (TI): Normalization and subtraction of cap-trapper-selected
 cDNAs to prepare full-length cDNA libraries for rapid
 discovery of new genes
 JOURNAL (SO): Genome Res., 10 (10), 1617-1630 (2000)
 OTHER SOURCE (OS): CA 134:305920
 REFERENCE: 3
 AUTHOR (AU): Shibata,K.; Itoh,M.; Aizawa,K.; Nagaoka,S.; Sasaki,N.;
 Carninci,P.; Konno,H.; Akiyama,J.; Nishi,K.;
 Kitsunai,T.; Tashiro,H.; Itoh,M.; Sumi,N.; Ishii,Y.;
 Nakamura,S.; Hazama,M.; Nishine,T.; Harada,A.;
 Yamamoto,R.; Matsumoto,H.; Sakaguchi,S.; Ikegami,T.;
 Kashiwagi,K.; Fujiwake,S.; Inoue,K.; Togawa,Y.;
 Izawa,M.; Ohara,E.; Watahiki,M.; Yoneda,Y.;
 Ishikawa,T.; Ozawa,K.; Tanaka,T.; Matsuura,S.;
 Kawai,J.; Okazaki,Y.; Muramatsu,M.; Inoue,Y.; Kira,A.;
 Hayashizaki,Y.
 TITLE (TI): RIKEN integrated sequence analysis (RISA)
 system--384-format sequencing pipeline with 384
 multicapillary sequencer
 JOURNAL (SO): Genome Res., 10 (11), 1757-1771 (2000)
 REFERENCE: 4
 AUTHOR (AU): The RIKEN Genome Exploration Research Group Phase II
 Team; the FANTOM Consortium.
 TITLE (TI): Functional annotation of a full-length mouse cDNA
 collection
 JOURNAL (SO): Nature, 409, 685-690 (2001)
 OTHER SOURCE (OS): CA 134:203311
 REFERENCE: 5
 AUTHOR (AU): The FANTOM Consortium; the RIKEN Genome Exploration
 Research Group Phase I & II Team.
 TITLE (TI): Analysis of the mouse transcriptome based on functional
 annotation of 60,770 full-length cDNAs
 JOURNAL (SO): Nature, 420, 563-573 (2002)
 OTHER SOURCE (OS): CA 138:131939
 REFERENCE: 6 (bases 1 to 4374)
 AUTHOR (AU): Adachi,J.; Aizawa,K.; Akimura,T.; Arakawa,T.; Bono,H.;
 Carninci,P.; Fukuda,S.; Furuno,M.; Hanagaki,T.;
 Hara,A.; Hashizume,W.; Hayashida,K.; Hayatsu,N.;
 Hiramoto,K.; Hiraoka,T.; Hirozane,T.; Hori,F.;
 Imotani,K.; Ishii,Y.; Itoh,M.; Kagawa,I.; Kasukawa,T.;
 Katoh,H.; Kawai,J.; Kojima,Y.; Kondo,S.; Konno,H.;
 Kouda,M.; Koya,S.; Kurihara,C.; Matsuyama,T.;
 Miyazaki,A.; Murata,M.; Nakamura,M.; Nishi,K.;
 Nomura,K.; Numazaki,R.; Ohno,M.; Ohsato,N.; Okazaki,Y.;
 Saito,R.; Saitoh,H.; Sakai,C.; Sakai,K.; Sakazume,N.;
 Sano,H.; Sasaki,D.; Shibata,K.; Shinagawa,A.;
 Shiraki,T.; Sogabe,Y.; Tagami,M.; Tagawa,A.;
 Takahashi,F.; Takaku-Akahira,S.; Takeda,Y.; Tanaka,T.;
 Tomaru,A.; Toya,T.; Yasunishi,A.; Muramatsu,M.;
 Hayashizaki,Y.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (16-JUL-2001) Yoshihide Hayashizaki, The
 Institute of Physical and Chemical Research (RIKEN),
 Laboratory for Genome Exploration Research Group, RIKEN
 Genomic Sciences Center (GSC), RIKEN Yokohama
 Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-
 res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>,
 Tel:81-45-503-9222, Fax:81-45-503-9216)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4374	/organism="Mus musculus" /mol-type="mRNA" /strain="C57BL/6J" /db-xref="FANTOM-DB:6030405B10" /db-xref="taxon:10090" /clone="6030405B10" /sex="male" /tissue-type="testis"

misc-feature 1..4374

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/clone-lib="RIKEN full-length  
enriched mouse cDNA library"  
/dev-stage="13 days embryo"  
/note="weakly similar to  
SEMAPHORIN 6A PRECURSOR  
(SEMAPHORIN VIA) (SEMA VIA)  
(SEMAPHORIN Q) (SEMA Q) [Mus  
musculus] (SWISSPROT|O35464,  
evidence: FASTY, 60.6%ID,  
64.8%length, match=1719)"
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SEQUENCE (SEQ):

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3901 tctgtgtact tgccggaaac gaaggggaggt cctgctcaact ccatttcttt cgtttgaagc
3961 agaaggggatg tggtagccagg gaaggctccc ttaccaggta taaagagctg atacagtaact
4021 cagaagactg aacaaatact tgaaaatggg ttcaatgttag actgccattc tgggtggct
4081 tccccattaaa tggtaaacatt ttaatatgtt tgcatcacc ttgccttttgc cacaatgtc
4141 aaaatggaaa gatgggaatg tctcaaaaca aaatgagctt ggagattacc aagcagtttgc
4201 ctgaaaattc aatctttgac ccaaactgtt gcaatttta ttttctgttttgc gtggcactgt
4261 tttgttttat tttttttgtt ttgtttttgtt tttcaatgtt accaacaac tatgttaaga
4321 gagggggcggag tgggtgtgtg tgggtgtgtg tgggtgtgtg tgggtgtgtg agag

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L4 ANSWER 54 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): CA341055 GenBank (R)
GenBank ACC. NO. (GBN): CA341055
GenBank VERSION (VER): CA341055.1 GI:24559151
CAS REGISTRY NO. (RN): 472461-69-1
SEQUENCE LENGTH (SQL): 477
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 4 Nov 2002
DEFINITION (DEF): haa83a04.y1 Fugu hgmpG adult eye Takifugu rubripes cDNA
clone 6360486 5' similar to TR:035464 035464
SEMAPHORIN ***VIA*** PRECURSOR. ;, mRNA
sequence.
KEYWORDS (ST): EST
SOURCE: Takifugu rubripes
ORGANISM (ORGN): Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Actinopterygii; Neopterygii; Teleostei;
Euteleostei; Neoteleostei; Acanthomorpha;
Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu
NUCLEIC ACID COUNT (NA): 108 a 118 c 144 g 107 t
COMMENT:
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zebrafish@watson.wustl.edu
Library materials and construction by Greg Elgar (UK MRC HGMP-RC).
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Fugu clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: T3 ET from Amersham.
REFERENCE:
AUTHOR (AU): 1 (bases 1 to 477)
Clark,M.; Johnson,S.L.; Lehrach,H.; Lee,R.; Li,F.;
Marra,M.; Eddy,S.y; Hillier,L.; Kucaba,T.; Martin,J.;
Beck,C.; Wylie,T.; Underwood,K.; Steptoe,M.;
Theising,B.; Allen,M.; Bowers,Y.; Person,B.;
Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.;
Ritter,E.; Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.;
McCann,R.; Wilson,R.
TITLE (TI): WashU Zebrafish EST Project 1998
JOURNAL (SO): Unpublished (1998)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..477	/organism="Takifugu rubripes" /db-xref="taxon:31033" /clone="6360486" /clone-lib="Fugu hgmpG adult eye" /dev-stage="adult" /lab-host="DH10B (T1-resistant)" /note="Organ: eye; Vector: pBluescript II KS (Stratagene); Site-1: XbaI; Site-2: EcoRI; Library is oligo-dT primed and directionally cloned using cDNA prepared with the Stratagene cDNA synthesis kit. Tissue source: adult eye. Library materials and construction by Greg Elgar (UK MRC HGMP-RC)."

SEQUENCE (SEQ):

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1 cggctcctgg gacgctcg tcaccgaggg gagtttcgaa atcaaaccag
61 cccgttgc tccctccga gagtgattt ccgatggata tttgctgt aagagggtgt
121 atttcagcgc ggcataac aaaaagaagc gcaagagaaa agtagcgctc gtattgttgc
181 tgtgccgaag cgggcgcgt ctgaactgccc gtgagcgccg tctcatggat tactaaagg
241 cagagttgt aaccactcc gagacgcatt cattcatgag ctgaaggctg agaggattct
301 gtagcagagg accagcgca gcggcggcgg cggctgtggc agtgggttg cgaccatgag
361 gtcagaggcc ttgttactct acttcacgtc actgcagata gctggggcgg gcttccccga
421 ggacagtga a cctattagca tctcgacag caactacaca aagcgtatc cggcggtt

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L4 ANSWER 55 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BC032619 GenBank (R)
 GenBank ACC. NO. (GBN): BC032619
 GenBank VERSION (VER): BC032619.1 GI:22749800
 CAS REGISTRY NO. (RN): 453031-06-6
 SEQUENCE LENGTH (SQL): 6875
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): High-Throughput CDNA Sequencing
 DATE (DATE): 4 Mar 2003
 DEFINITION (DEF): Homo sapiens, similar to sema domain, transmembrane
 domain (TM), and cytoplasmic domain, (***semaphorin***) ***6A*** , clone IMAGE:5578066,
 mRNA.

KEYWORDS (ST): HTC
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 1784 a 1795 c 1592 g 1704 t

COMMENT:

Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
 Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
 Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghghi,P.,
 Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
 Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
 McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
 Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,L.-H. and Green,E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 69 Row: o Column: 4
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 11991659
 This clone has the following problem: retained intron.

REFERENCE: 1 (bases 1 to 6875)
 AUTHOR (AU): Strausberg,R.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (06-JUN-2002) National Institutes of Health,
 Mammalian Gene Collection (MGC), Cancer Genomics
 Office, National Cancer Institute, 31 Center Drive,
 Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..6875	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:5578066" /tissue-type="Skin, melanotic melanoma." /clone-lib="NIH-MGC-72" /lab-host="DH10B" /note="Vector: pCMV-SPORT6"

SEQUENCE (SEQ):

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 121 gtagtgagcg gcacgggggtt aggtgcagc caactccgtt ccccgccgac tcggctgccc
 181 aggcgctcggt aacccagcag cggcgctcct ccgcgggtcc ggtcggccgc gatgcccgt
 241 tagcagcggt tagcagcggt cagcatcacc acaccccggtt caccgcgtt ccggccgcag
 301 agccgggcca gagccttgc cccctgcctt agccccccacc ccgcggcccg ccctgaattt
 361 acttgttaat cggcgacac accaccaagg ggactcaccg gagtggaaatc caagtgaat
 421 ttggattttgg agaagagttt cttgaacatt tacccttcc tttgtgggtt ttcttttct
 481 ttttcttctt ttttttttgc gttttttttt tcctctcccc ttctccgcgt gtcattggag
 541 atgaacacat cgcgtttgc tcccgaaaag tagtcgcgc gactatttcc cccaaagaga
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 1441 tgaagaagaacc atactttgtt caagccgtgg attacggaga ttatatctac ttcttctca
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 1561 tttgtttagaa tgatatggga ggatctcaaa gaggatcttgg gaggatctca tttttatttc
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 3061 ccccagagtc aaccccaacg ctgcagcaga agcggaaagcc cagccgcggc agccgc当地
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 3181 ctgttattttt cccatccat cccctgcggg cctcccccac ccacatcccccc agcgtgggtgg
 3241 tcctgc当地t cccatccat cccatccat cccatccat atgagttacgt ggaccacccccc
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 3361 aacatctcag cagcaagat cccatccat cccatccat ggggttacgt tggggatgggg
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 3601 acaacactaa cccatccat cccatccat
 3661 acaacccggcc cccatccat cccatccat
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 4141 accccacaaaaa cccatccat cccatccat
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 4261 gaacagaaac cccatccat cccatccat
 4321 ttccaaacccctt cccatccat cccatccat
 4381 aaaaagaattt cccatccat cccatccat

4441 caaatactgt gaaatgcccc ccagtgttac agctttctgt tgccagcagat aaatgccatg
4501 ttggccaact atgtcataga tttctgttcc tcctctctt taatgaaata acgtgaccgt
4561 taaccaagt aactctttat ttattgttca ccctttttt ccttaaggaa aggacttcc
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5641 ctggaggag tctccaagcc atgtgcacag cacacacgtg cagtgcacac aaagaaatga
5701 catggaaata gatgcaggca ggctgggtcc tgctgtgatt aacgagtaac tccaagtaca
5761 aggccgacca caatggatgc tgcaaaaacg ttgactggg caaaggatttttatt
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6001 ggtggctctt ttgtctgtt ttatttccag ttcatcttc tgggttttagt tttgtcttta
6061 aaaagaattt aaaaaaaagac tgacaatgac agttttgagt tggatagtga aaaagtggag
6121 cctccataat cagtgtgggt gccttcagac ctgagttactt agctgagggt gggtgagagc
6181 ccttggttcc aaaagtccat tagttttgt gttgtttagg agtaggtgt tttgttttt
6241 tttactttt ttttttttgg cttttgtat ggaatccatg ttcacatctt gtgaactctg
6301 tctcctgaaa cctcgaagta tttccctagaa ctttgcattttt tttttttttt
6361 ctctagaaat gcagaaatta ggaagggtat ggggtctgtat cccctgccc cttctttcc
6421 catgttgac tcccggaggt actggcagtg cagcacccat cattgacgtt a cggctgtc
6481 ttgtccagt tttgttaggca tcactgcctc agctgttaag gagacctgtg tcaaaactta
6541 catccacatt cctacaccccc cacaacccat cacttctgtt gttaacccta aaataccac
6601 atgtatttgg ctggtcttgc gatTTTAAAGT atttctcccc agtttttttcc cccactgtgt
6661 gtggggggag ggtccataaa cccgagtgtg ctttgcctt ccacccttgc tagacactgg
6721 tagatgcaac aaactcagat ttatTTTGT tgtaaagggt taaaatattt gtatgtcac
6781 caattttcct tccatcttca catcccctaa catctgttcc acgacttaat gtatgttga
6841 agaaaaagaaa aaagaaaaaa aaaaaaaaaa aaaaa

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LOCUS (LOC): BM182435 GenBank (R)
GenBank ACC. NO. (GBN): BM182435
GenBank VERSION (VER): BM182435.1 GI:17513393
CAS REGISTRY NO. (RN): 376921-60-7
SEQUENCE LENGTH (SQL): 717
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 11 Dec 2001
DEFINITION (DEF): fv61g11.x1 Sugano SJD adult male Danio rerio cDNA clone
5413076 3' similar to TR:035464 035464
SEMAPHORIN ***VIA*** PRECURSOR. ;contains
element LTR3 repetitive element ;, mRNA sequence.
zebrafish.
ORGANISM (ORGN): Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Actinopterygii; Neopterygii; Teleostei;
Ostariophysi; Cypriniformes ; Cyprinidae; Danio

NUCLEIC ACID COUNT (NA): 153 a 141 c 195 g 228 t

COMMENT:

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.
Consortium/LLNL, send email to: info@image.llnl.gov

Seq primer: T7 from Gibco

High quality sequence stop: 463.

REFERENCE: 1 (bases 1 to 717)

AUTHOR (AU): Clark,M.; Johnson,S.L.; Lehrach,H.; Lee,R.; Li,F.;
 Marra,M.; Eddy,S.y; Hillier,L.; Kucaba,T.; Martin,J.;
 Beck,C.; Wylie,T.; Underwood,K.; Steptoe,M.;
 Theising,B.; Allen,M.; Bowers,Y.; Person,B.;
 Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.;
 Ritter,E.; Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.;
 McCann,R.; Wilson,R.
 TITLE (TI): WashU Zebrafish EST Project 1998
 JOURNAL (SO): Unpublished (1998)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..717	<code>/organism="Danio rerio"</code> <code>/db-xref="taxon:7955"</code> <code>/clone="5413076"</code> <code>/clone-lib="Sugano SJD adult male"</code> <code>/sex="male"</code> <code>/tissue-type="whole body"</code> <code>/dev-stage="adult"</code> <code>/lab-host="DH10B (phage resistant)"</code> <code>/note="Vector: pME18S-FL3; Site-1: DraIII (CACCATGTG); Site-2: DraIII (CACTGTGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGCCCTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA. "</code>

SEQUENCE (SEQ):

```

1 tttttttttt tttttttttc aatgaaagaa accagattta ttgacaataa ccaccctcca
 61 ccactgcata atcattcagt gtgcaccata ataacatccc atctcttata tttacactat
121 atacacacta tattttacaca ctgcagtcata caatgtgctg gtattctgac ccctgagtg
181 gtgggctcag ttgtgtgttt gtttgggtgt gtcatgtgaa cacatggtca gtagttgtgt
241 ttgtgtcatg tgatcgcggg gtcagtagtt gtgtgtcggt atcgcgggt tagtagttgc
301 atgtgtgtgt tttgtgacca gtgtgtccca acagggtcaa tagttgtgt tttatggcat
361 gtgactgtgt ggtcaatagt tttgtgtgtat atgtgagcgc gaggtcaga tttttgtgt
421 tttgtgtgtgt tttgtgtgtgt tttgtgtgtt ggtcaaaatc ttcaagcacgc gtccgtcttc
481 agagccccaga aacactacag tgcgggttctt atgaggccca gcagcagtgt ccaccacaa
541 ctgagtctgc ttataccctgc tggcggtgtt ggtgatcagc ggtggctgt tgactgacgg
601 cacgtctcc tccatcagcg ggtgtgtttt gatgaacacac agcacagatg ctggaaactg
661 aacagaagag gaataggagg aggcagaacc ctcacgtca cacaaccgt gggttgg

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L4 ANSWER 57 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BM180699 GenBank (R)
 GenBank ACC. NO. (GBN): BM180699
 GenBank VERSION (VER): BM180699.1 GI:17404770
 CAS REGISTRY NO. (RN): 376286-68-9
 SEQUENCE LENGTH (SQL): 561
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 7 Dec 2001
 DEFINITION (DEF): daj83c05.y1 NICHD XGC Li1 Xenopus laevis cDNA clone
 IMAGE:5129457 5' similar to TR:035464 035464
 SEMAPHORIN ***VIA*** PRECURSOR. ;, mRNA
 sequence.

SOURCE: African clawed frog.
 ORGANISM (ORGN): Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Amphibia; Batrachia; Anura;

Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus

NUCLEIC ACID COUNT (NA): 133 a 126 c 115 g 187 t

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Seq primer: -40RP from Gibco

High quality sequence stop: 444.

REFERENCE: 1 (bases 1 to 561)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..561	/organism="Xenopus laevis" /db-xref="taxon:8355" /clone="IMAGE:5129457" /clone-lib="NICHD XGC Li1" /lab-host="DH10B (phage-resistant)" /note="Organ: liver; Vector: pCMV-SPORT6; Site-1: NotI; Site-2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.4 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."

SEQUENCE (SEQ):

1 gctgcaagcc tcctgcccct ttgtctgttt ggagatagcg aatgtgcttt tgcgtgttga
61 aatagaaagc taagcagact ttctgaaaat tatattttgc agacatgtga tcttccagg
121 gattatagc ttgtcttcaa atggcacatt cttatcttcc agaacacatg gttctataat
181 gaaattttc ttttggggc atttcttctt aatgtatgtt ggcatttcg tattccctag
241 cgcatcccg catttttaac ctgataacaac aaaaccttgt tttttccct ctctagggtgg
301 ttttcccaag agtcgcccag gtgtgcaaaa atgacatggg gggatctcg agggtacttg
361 aaaaacagtg gacatcttc ctaaaagctc gactgaattt ctcgggtccct ggggattccc
421 atttcttattt caacattttg caagctgtt a cagacgtcat tcataatcaat ggccgagacg
481 ttgtcttggc tacttttca acaccgtaca acagcatccc cggtctgtct gtttgtgcct
541 atgatatggc tgacatcgct a

L4 ANSWER 58 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BG816002 GenBank (R)

GenBank ACC. NO. (GBN): BG816002

GenBank VERSION (VER): BG816002.1 GI:14186982

CAS REGISTRY NO. (RN): 338672-75-6

SEQUENCE LENGTH (SQL): 589

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 22 May 2001

DEFINITION (DEF): dad39a04.y1 Wellcome CRC pCS107 tropicalis St10-12
Silurana tropicalis cDNA clone IMAGE:4461607 5' similar
to TR:035464 035464 ***SEMAPHORIN*** ***VIA***
PRECURSOR. ;, mRNA sequence.

SOURCE: western clawed frog.

ORGANISM (ORGN): Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi; Amphibia; Batrachia; Anura;

Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; silurana

NUCLEIC ACID COUNT (NA): 154 a 125 c 145 g 165 t

COMMENT:

Contact: Sandy Clifton, Ph.D.

WashU Xenopus EST project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

High quality sequence stop: 513.

REFERENCE: 1 (bases 1 to 589)

AUTHOR (AU): Clifton,S.; Johnson,S.L.; Blumberg,B.; Song,J.; Hillier,L.; Pape,D.; Martin,J.; Wylie,T.; Underwood,K.; Theising,B.; Bowers,Y.; Person,B.M.; Gibbons,M.; Harvey,N.; Ritter,E.; Jackson,Y.; McCann,R.; Waterston,R.; Wilson,R.

TITLE (TI): WashU Xenopus EST project, 1999

JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..589	/organism="Silurana tropicalis" /db-xref="taxon:8364" /clone="IMAGE:4461607" /clone-lib="Wellcome CRC pCS107 tropicalis St10-12" /tissue-type="whole embryo, stages 10-12" /lab-host="DH10B (phage-resistant)" /note="Vector: pCS107; Site-1: NotI; Site-2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Average insert size 1.5 kb, range 0.5-4 kb. Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute). "

SEQUENCE (SEQ):

1 cccggggcct tgggtgtgtc tttctctggc tgcattgtca gactgccttt gagccgctgt
61 gagcgatacg gatcatgcaaa aaagtcttgtt attgggtgcaaa gggatcctta ttgtggctgg
121 ctgaaccatg agtcctgcgg aagagtggaa ccgggcgtgt tttttggta tgaacaggat
181 gtggaaatacg gcaacacagt acagcttggc gactgtcatg acattttgcc tactgcaact
241 acaccagatt acaaataattt tggcgatcca acatctgaca ttgaagttcc ttctacttct
301 gtaaccacca caagtagcccc agttatTTTA ccttaaagtga ttggttcctg gaaaccacaga
361 atgactggct cacggaaatt tatataccaa gatgacccaa acacccaga gtatattgtat
421 ccgttaacag gtgtccaaaa ggggtacgg tgggaagttt agtcaggaga cgccaaaccaa
481 atggccatca tgaatgtttt gatcacctgc gttcttgct cttttgtgtc cggagctttc
541 atcgcaggag tgatagttt ctgtacagg gagatgtttg taaggaaaa

L4 ANSWER 59 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AK027867 GenBank (R)

GenBank ACC. NO. (GBN): AK027867

GenBank VERSION (VER): AK027867.1 GI:14042853

CAS REGISTRY NO. (RN): 390638-15-0

SEQUENCE LENGTH (SQL): 6060

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Primates

DATE (DATE): 30 Jan 2004

DEFINITION (DEF): Homo sapiens cDNA FLJ14961 fis, clone PLACE4000230,
highly similar to *Mus musculus* ***semaphorin***
VIA mRNA.

KEYWORDS (ST): oligo capping; fis (full insert sequence)

SOURCE: Homo sapiens (human)

ORGANISM (ORGN): Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

COMMENT:

NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

REFERENCE:

1

AUTHOR (AU):

Ota,T.; Suzuki,Y.; Nishikawa,T.; Otsuki,T.;
Sugiyama,T.; Irie,R.; Wakamatsu,A.; Hayashi,K.;
Sato,H.; Nagai,K.; Kimura,K.; Makita,H.; Sekine,M.;
Obayashi,M.; Nishi,T.; Shibahara,T.; Tanaka,T.;
Ishii,S.; Yamamoto,J.; Saito,K.; Kawai,Y.; Isono,Y.;
Nakamura,Y.; Nagahari,K.; Murakami,K.; Yasuda,T.;
Iwayanagi,T.; Wagatsuma,M.; Shiratori,A.; Sudo,H.;
Hosoiri,T.; Kaku,Y.; Kodaira,H.; Kondo,H.; Sugawara,M.;
Takahashi,M.; Kanda,K.; Yokoi,T.; Furuya,T.;
Kikkawa,E.; Omura,Y.; Abe,K.; Kamihara,K.; Katsuta,N.;
Sato,K.; Tanikawa,M.; Yamazaki,M.; Ninomiya,K.;
Ishibashi,T.; Yamashita,H.; Murakawa,K.; Fujimori,K.;
Tanai,H.; Kimata,M.; Watanabe,M.; Hiraoka,S.; Chiba,Y.;
Ishida,S.; Ono,Y.; Takiguchi,S.; Watanabe,S.;
Yosida,M.; Hotuta,T.; Kusano,J.; Kanehori,K.;
Takahashi-Fujii,A.; Hara,H.; Tanase,T.; Nomura,Y.;
Togiya,S.; Komai,F.; Hara,R.; Takeuchi,K.; Arita,M.;
Imose,N.; Musashino,K.; Yuuki,H.; Oshima,A.; Sasaki,N.;
Aotsuka,S.; Yoshikawa,Y.; Matsunawa,H.; Ichihara,T.;
Shiohata,N.; Sano,S.; Moriya,S.; Momiyama,H.; Satoh,N.;
Takami,S.; Terashima,Y.; Suzuki,O.; Nakagawa,S.;
Senoh,A.; Mizoguchi,H.; Goto,Y.; Shimizu,F.; Wakebe,H.;
Hishigaki,H.; Watanabe,T.; Sugiyama,A.; Takemoto,M.;
Kawakami,B.; Yamazaki,M.; Watanabe,K.; Kumagai,A.;
Itakura,S.; Fukuzumi,Y.; Fujimori,Y.; Komiyama,M.;
Tashiro,H.; Tanigami,A.; Fujiwara,T.; Ono,T.;
Yamada,K.; Fujii,Y.; Ozaki,K.; Hirao,M.; Ohmori,Y.;
Kawabata,A.; Hikiji,T.; Kobatake,N.; Inagaki,H.;
Ikeda,Y.; Okamoto,S.; Okitani,R.; Kawakami,T.;
Noguchi,S.; Itoh,T.; Shigeta,K.; Senba,T.;
Matsumura,K.; Nakajima,Y.; Mizuno,T.; Morinaga,M.;
Sasaki,M.; Togashi,T.; Oyama,M.; Hata,H.; Watanabe,M.;
Komatsu,T.; Mizushima-Sugano,J.; Satoh,T.; Shirai,Y.;
Takahashi,Y.; Nakagawa,K.; Okumura,K.; Nagase,T.;
Nomura,N.; Kikuchi,H.; Masuho,Y.; Yamashita,R.;
Nakai,K.; Yada,T.; Nakamura,Y.; Ohara,O.; Isogai,T.;
Sugano,S.

TITLE (TI):

Complete sequencing and characterization of 21,243
full-length human cDNAs

JOURNAL (SO):

Nat. Genet., 36 (1), 40-45 (2004)

OTHER SOURCE (OS):

CA 140:158332

2

REFERENCE:

AUTHOR (AU):

Isogai,T.; Ota,T.; Hayashi,K.; Sugiyama,T.; Otsuki,T.;
Suzuki,Y.; Nishikawa,T.; Nagai,K.; Sugano,S.;
Takahashi-Fujii,A.; Hara,H.; Tanase,T.; Nomura,Y.;
Togiya,S.; Komai,F.; Hara,R.; Takeuchi,K.; Arita,M.;
Nabekura,T.; Ishii,S.; Kawai,Y.; Saito,K.; Yamamoto,J.;
Wakamatsu,A.; Nakamura,Y.; Nagahari,K.; Masuho,Y.;
Oshima,A.

TITLE (TI):

NEDO human cDNA sequencing project

JOURNAL (SO):

Unpublished

REFERENCE:

3 (bases 1 to 6060)

AUTHOR (AU):

Isogai,T.; Otsuki,T.

TITLE (TI):

Direct Submission

JOURNAL (SO):

Submitted (10-MAY-2001) Takao Isogai, Helix Research
Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,
Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
Tel:81-438-52-3975, Fax:81-438-52-3986)

FEATURES (FEAT):

	Feature Key	Location	Qualifier
source	1..6060		/organism="Homo sapiens" /mol-type="mRNA" /db-xref="taxon:9606" /clone="PLACE4000230" /tissue-type="placenta" /clone-lib="PLACE4" /note="cloning vector: pME18SFL3" /note="unnamed protein product" /codon-start=1 /protein-id="BAB55418.1" /db-xref="GI:14042854" /translation="MIMNGTLYIAARDHIYTVDI DTSHTEEIYCSKKLTWKSQRQADVD TCRMKGKHKDECHNFIKVLLKKNDDALFVCGTNA
CDS	89..1345		

FNPSCRNYKMDTLEPFGDEFGMA
 RCPYDAKHANVALFADGKLYSATVTDFAIDAVI
 YRSLGESPTLRTVKHDSKWLEPY
 FVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVA
 QVCKNDMGGSQRVLEKQWTSFLKA
 RLNCSPVGDSHFYFNILQAVTDVIRINGRDVVA
 TFSTPYNSIPGSACAYDMLDIAS
 VFTGRFKEQKSPDSTWTPVDPERVPKPRPGCCAG
 SSSLERYATSNEFPDDTLNFIKTH
 PLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAA
 GPYQNHTVVFLGSEKGIIILKFLAR
 IGNSGFLNDSLLEEMSVYNSEKMQL"

SEQUENCE (SEQ):

1 caactataca aaacagtatc cggtgtttgt gggccacaag ccaggacgga acaccacaca
 61 gaggcacagg ctggacatcc aggtgattat gatcatgaac ggaaccctct acattgctgc
 121 taggaccat atttatactg ttgatataga cacaatcacac acgaaagaaa tttattttag
 181 caaaaaactg acatggaaat ctagacaggc cgatgttagac acatgcagaa tgaagggaaa
 241 acataaggat gagtgcacaca actttattaa agttcttcta aagaaaaacg atgatgcatt
 301 gtttgtctgt ggaactaaatg ccttcaaccc ttccctgcaga aactataaga tggatacatt
 361 ggaaccattc ggggatgaat tcagcggaaat ggcacatgc ccatatgtat ccaaacatgc
 421 caacgttgca ctgtttgcag atggaaaact atactcagcc acagtactg acttccttgc
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 541 cgattcaaaa tggttgaag aaccataactt tgtaaagcc gtgattacg gagattatat
 601 ctacttcttc ttcaaggaaa tagcagtggaa gtataacacc atggaaagg tagttttccc
 661 aagagtggct cagggttgtt agaatgatata gggaggatct caaagagtcc tggagaaaca
 721 gtggacgtcg ttccctgaagg cgcgcgttgg ctgctcaattt ccttggagact ctcattttta
 781 tttcaacatt ctccaggcgg ttacagatgt gattcgtatc aacggggcgtg atgttgtcct
 841 ggcaacgttt tctacaccc ttacagatgtt ccctgggtct gcagtctgtg cctatgacat
 901 gcttgacatt gccagtgttt ttacttggag attcaagaa cagaagtctc ctgattccac
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 1081 caagacgcac ccgcctcatgg atgaggcagt gcccctccatc ttcaacaggc catggttcct
 1141 gagaacaatg gtcagatacc gccttaccaa aattgcagtg gacacagctg ctggggccata
 1201 tcagaatcac actgtgggtt ttcttggatc agagaaggaa atcatcttgc agtttttggc
 1261 cagaatagga aatagtgggtt ttctaaatgaa cagcctttt ctggaggaga tgagtgttta
 1321 caactctgaa aaaatgcgac tatgtatggag tcgaagacaa aaggatcatg ggcatgcagc
 1381 tggacagagc aagcagctct ctgtatgtt cgttctctac ctgtgtgata aaggttcccc
 1441 ttggccgtgt tgaacgcacat gggaaagtgtt aaaaaaaacct gtattgcctc cagagaccca
 1501 tattgtggat ggataaaagga aggtgggtcc tgcagccatt tatttgcctc cagcagactg
 1561 acttttgcgc aggacataga gcgtggcaat acagatgtc tggggactg tcacaattcc
 1621 ttttgtggcac tgaatgggc ttcttagttcc cttttgcctc gcacaaccac atcagattcg
 1681 acggctcaag aggggtatga gtcttagggga ggaatgtcgg acttggaaagca tctgcttgac
 1741 tcacccgtaca gcacagaccc ttggggggca gtgtctttccataatccca agacaagaag
 1801 ggagtgtttt gggaaaggta ccttccaaaggc caccggcgc tgggtttccgt cacccttttgc
 1861 gccattgcag tcatacttgc ttctgtcatg gggggccgtct tcttgggcat caccgtctac
 1921 tgcgtctgtt atcatcgccg caaagacgtt gctgtgttgc agcacaaggaa gaaggagctc
 1981 acccaactcgc gcccggggctc catgagcggc gtccaccaacgc tcagcggcct tttggggac
 2041 actcaatccg aagacccaaa gcccggggcc atcctcacgc cactcatgca caacggcaag
 2101 ctcgcccactc ccggcaacac ggccaagatg ctcatccatc cagactagca ccacctggac
 2161 ctgacggcccc tccccacccc agatcaacc ccaacgcgtc agcagaagcg gaagcccac
 2221 cgcggcagcc gcgagttggaa gaggaaaccat aacccatcatca atgcctgcac aaaggacatg
 2281 ccccccattgg gctccctgtt gattttccacg gacctggccc tggggccctc ccccgccac
 2341 atccccagcg tgggtgttcc gcccattcagc cagcagggtt accagcatga gtacgtggac
 2401 cagcccaaaa tgagcgaggt ggcccagatg gcgctggagg accaggccgc cacactggag
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 2521 gagaacctgg acaggctgccc ccccaaaatgg ccacagcggg aggccctccct ggtcccccc
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 2641 tacgggggtt actataagag gagttttccctt acgaactcgc tcacgagaag ccaccaggcc
 2701 accactctca aaagaaaacaa cactaactcc tccaatttctt ctccacctctc cagaaaccag
 2761 agctttggca ggggagacaa cccggccccc gccccgcaga ggggtggactc catccaggtt
 2821 cacagctccc agccatctgg ccaggccgtg actgtctcgaa ggcagcccg cctcaacgc
 2881 tacaactcac tgacaagggtt ggggtgttgc cgtacgcctt cgttcaagcc ggacgttaccc
 2941 cccaaacccat ctttgcctt ctttccacat tccatgtatc ccaatgtgc gtgtacataa
 3001 tcccaggggg aggggggttgc gtttgcaccc agcaggcaag ggcagggttgc cgctcagctc
 3061 agcaagggtt tcaacttgcctt cggatccca ccagaccaag aaggccctgcg gcagagccga
 3121 ggacgctggg tccttccttc tgggacacag ggggtacttcc gaaaacttggg ccgcgtgg
 3181 tggtaaggt ttgcacccggc ggggacttcc ttttccatc ttccatccact ttcccccaca
 3241 ccctacaaca ggtcgacccccc aaaaaaactt ctagttatca tcacaaacat gagccaaaag
 3301 cacataccat ccccatcccc caccacacca cacaacacaca cacaacacaca catgcacaca
 3361 acacatacac acacacgcac agagggttgc acggaaacttgc cacaacttca
 3421 cgggacgtgg ccagacttgg attgcgttcc aacctgcacca acacaaatac attttttaaa
 3481 atcaagaaaa tttaaaaaga aaaaaaaaaa agaatttatttca actcagactt
 3541 taacaatggc agaagggttac tatgcgcaccc tactgtggaaa tgccggccag tgtttac
 3601 ttctgttgca gcagataaaat gccatgttgg gcaactatgtt catagatttc tgctccctc
 3661 ctcttttaat gaaataacgt gaccgttaac gcaagtaact ctttattttat tgttcaccct

3721 tttttccctt aaggaaagga ctcttccaaa tatcatccta tgaacagctc ttcagaaagc
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L4 ANSWER 60 OF 86

GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AK027654 GenBank (R)
 GenBank ACC. NO. (GBN): AK027654
 GenBank VERSION (VER): AK027654.1 GI:14042491
 CAS REGISTRY NO. (RN): 390635-08-2
 SEQUENCE LENGTH (SQL): 2306
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 30 Jan 2004
 DEFINITION (DEF): Homo sapiens cDNA FLJ14748 fis, clone NT2RP3002869,
 highly similar to *Mus musculus* ***Semaphorin***
 VIA mRNA.
 KEYWORDS (ST): oligo capping; fis (full insert sequence)
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

COMMENT:

NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction,
 5'- & 3'-end one pass sequencing and clone selection: Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.

REFERENCE: 1
 AUTHOR (AU): ota,T.; Suzuki,Y.; Nishikawa,T.; Otsuki,T.;
 Sugiyama,T.; Irie,R.; Wakamatsu,A.; Hayashi,K.;
 Sato,H.; Nagai,K.; Kimura,K.; Makita,H.; Sekine,M.;
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 Sugano,S.

TITLE (TI): Complete sequencing and characterization of 21,243
full-length human cDNAs

JOURNAL (SO): Nat. Genet., 36 (1), 40-45 (2004)

OTHER SOURCE (OS): CA 140:158332

REFERENCE:

AUTHOR (AU): Isogai,T.; Ota,T.; Hayashi,K.; Sugiyama,T.; Otsuki,T.;
 Suzuki,Y.; Nishikawa,T.; Nagai,K.; Sugano,S.;
 Shiratori,A.; Sudo,H.; Wagatsuma,M.; Hosoiri,T.;
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 Ninomiya,K.; Iwayanagi,T.

TITLE (TI): NEDO human cDNA sequencing project

JOURNAL (SO): Unpublished

REFERENCE:

AUTHOR (AU): Isogai,T.; Otsuki,T.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (10-MAY-2001) Takao Isogai, Helix Research
 Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,
 Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
 Tel:81-438-52-3975, Fax:81-438-52-3986)

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L4 ANSWER 61 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AK027501 GenBank (R)
 GenBank ACC. NO. (GBN): AK027501
 GenBank VERSION (VER): AK027501.1 GI:14042222
 CAS REGISTRY NO. (RN): 390634-60-3
 SEQUENCE LENGTH (SQL): 3041
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 30 Jan 2004
 DEFINITION (DEF): Homo sapiens cDNA FLJ14595 fis, clone NT2RM4002194,
 highly similar to Mus musculus ***semaphorin***
 VIA mRNA.
 KEYWORDS (ST): oligo capping; fis (full insert sequence)
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

COMMENT:

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

REFERENCE:

AUTHOR (AU):

1
 Ota,T.; Suzuki,Y.; Nishikawa,T.; Otsuki,T.;
 Sugiyama,T.; Irie,R.; Wakamatsu,A.; Hayashi,K.;
 Sato,H.; Nagai,K.; Kimura,K.; Makita,H.; Sekine,M.;
 Obayashi,M.; Nishi,T.; Shibahara,T.; Tanaka,T.;
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TITLE (TI):

Complete sequencing and characterization of 21,243
 full-length human cDNAs

JOURNAL (SO):

Nat. Genet., 36 (1), 40-45 (2004)

OTHER SOURCE (OS):

CA 140:158332

REFERENCE:

AUTHOR (AU):

2
 Isogai,T.; Ota,T.; Hayashi,K.; Sugiyama,T.; Otsuki,T.;
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TITLE (TI):

NEDO human cDNA sequencing project

JOURNAL (SO):

Unpublished

REFERENCE:

AUTHOR (AU):

3 (bases 1 to 3041)

TITLE (TI):

Isogai,T.; Otsuki,T.

JOURNAL (SO):

Direct Submission

Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

FEATURES (FEAT):

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L4 ANSWER 62 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AK027471 GenBank (R)
GenBank ACC. NO. (GBN): AK027471
GenBank VERSION (VER): AK027471.1 GI:14042170
CAS REGISTRY NO. (RN): 390636-83-6
SEQUENCE LENGTH (SQL): 2293
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 30 Jan 2004
DEFINITION (DEF): Homo sapiens cDNA FLJ14565 fis, clone NT2RM4000233,
highly similar to Mus musculus ***semaphorin***
VIA mRNA.
KEYWORDS (ST): oligo capping; fis (full insert sequence)
SOURCE: Homo sapiens (human)
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

COMMENT:
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

REFERENCE: 1
AUTHOR (AU): Ota,T.; Suzuki,Y.; Nishikawa,T.; Otsuki,T.;
Sugiyama,T.; Irie,R.; Wakamatsu,A.; Hayashi,K.;
Sato,H.; Nagai,K.; Kimura,K.; Makita,H.; Sekine,M.;
Obayashi,M.; Nishi,T.; Shibahara,T.; Tanaka,T.;
Ishii,S.; Yamamoto,J.; Saito,K.; Kawai,Y.; Isono,Y.;
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Ishida,S.; Ono,Y.; Takiguchi,S.; Watanabe,S.;
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Matsumura,K.; Nakajima,Y.; Mizuno,T.; Morinaga,M.;
Sasaki,M.; Togashi,T.; Oyama,M.; Hata,H.; Watanabe,M.;
Komatsu,T.; Mizushima-Sugano,J.; Satoh,T.; Shirai,Y.;
Takahashi,Y.; Nakagawa,K.; Okumura,K.; Nagase,T.;

Nomura,N.; Kikuchi,H.; Masuho,Y.; Yamashita,R.;
Nakai,K.; Yada,T.; Nakamura,Y.; Ohara,O.; Isogai,T.;
Sugano,S.

TITLE (TI): Complete sequencing and characterization of 21,243
full-length human cDNAs

JOURNAL (SO): Nat. Genet., 36 (1), 40-45 (2004)

OTHER SOURCE (OS): CA 140:158332

2

Isogai,T.; Ota,T.; Hayashi,K.; Sugiyama,T.; Otsuki,T.;
Suzuki,Y.; Nishikawa,T.; Nagai,K.; Sugano,S.;
Shiratori,A.; Sudo,H.; Wagatsuma,M.; Hosoiri,T.;
Kaku,Y.; Kodaira,H.; Kondo,H.; Sugawara,M.;
Takahashi,M.; Chiba,Y.; Ishida,S.; Murakawa,K.; Ono,Y.;
Takiguchi,S.; Watanabe,S.; Kimura,K.; Murakami,K.;
Ishii,S.; Kawai,Y.; Saito,K.; Yamamoto,J.;
Wakamatsu,A.; Nakamura,Y.; Nagahari,K.; Masuho,Y.;
Ninomiya,K.; Iwayanagi,T.

TITLE (TI): NEDO human cDNA sequencing project

JOURNAL (SO): Unpublished

REFERENCE: 3 (bases 1 to 2293)

AUTHOR (AU): Isogai,T.; Otsuki,T.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (10-MAY-2001) Takao Isogai, Helix Research
Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,
Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
Tel:81-438-52-3975, Fax:81-438-52-3986)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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CDS	138..1826	

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L4 ANSWER 63 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AK027439 GenBank (R)
GenBank ACC. NO. (GBN): AK027439
GenBank VERSION (VER): AK027439.1 GI:14042113
CAS REGISTRY NO. (RN): 390631-17-1
SEQUENCE LENGTH (SQL): 2123
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 30 Jan 2004
DEFINITION (DEF): Homo sapiens cDNA FLJ14533 fis, clone NT2RM2000407,
moderately similar to *Mus musculus* ***semaphorin***
VIA mRNA.
KEYWORDS (ST): oligo capping; fis (full insert sequence)
SOURCE: Homo sapiens (human)
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

COMMENT:
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

REFERENCE: 1
AUTHOR (AU):
Ota,T.; Suzuki,Y.; Nishikawa,T.; Otsuki,T.;
Sugiyama,T.; Irie,R.; Wakamatsu,A.; Hayashi,K.;
Sato,H.; Nagai,K.; Kimura,K.; Makita,H.; Sekine,M.;
Obayashi,M.; Nishi,T.; Shibahara,T.; Tanaka,T.;
Ishii,S.; Yamamoto,J.; Saito,K.; Kawai,Y.; Isono,Y.;
Nakamura,Y.; Nagahari,K.; Murakami,K.; Yasuda,T.;
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Takahashi,M.; Kanda,K.; Yokoi,T.; Furuya,T.;
Kikkawa,E.; Omura,Y.; Abe,K.; Kamihara,K.; Katsuta,N.;
Sato,K.; Tanikawa,M.; Yamazaki,M.; Ninomiya,K.;
Ishibashi,T.; Yamashita,H.; Murakawa,K.; Fujimori,K.;
Tanai,H.; Kimata,M.; Watanabe,M.; Hiraoka,S.; Chiba,Y.;
Ishida,S.; Ono,Y.; Takiguchi,S.; Watanabe,S.;
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Togiya,S.; Komai,F.; Hara,R.; Takeuchi,K.; Arita,M.;
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Aotsuka,S.; Yoshikawa,Y.; Matsunawa,H.; Ichihara,T.;
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Takami,S.; Terashima,Y.; Suzuki,O.; Nakagawa,S.;
Senoh,A.; Mizoguchi,H.; Goto,Y.; Shimizu,F.; Wakebe,H.;
Hishigaki,H.; Watanabe,T.; Sugiyama,A.; Takemoto,M.;
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Tashiro,H.; Tanigami,A.; Fujiwara,T.; Ono,T.;
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Sasaki,M.; Togashi,T.; Oyama,M.; Hata,H.; Watanabe,M.;
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Nomura,N.; Kikuchi,H.; Masuho,Y.; Yamashita,R.;
Nakai,K.; Yada,T.; Nakamura,Y.; Ohara,O.; Isogai,T.;
Sugano,S.

TITLE (TI): Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL (SO): Nat. Genet., 36 (1), 40-45 (2004)
OTHER SOURCE (OS): CA 140:158332

REFERENCE:

AUTHOR (AU):

2

Isogai,T.; Ota,T.; Hayashi,K.; Sugiyama,T.; Otsuki,T.;
Suzuki,Y.; Nishikawa,T.; Nagai,K.; Sugano,S.;
Shiratori,A.; Sudo,H.; Wagatsuma,M.; Hosoiri,T.;
Kaku,Y.; Kodaira,H.; Kondo,H.; Sugawara,M.;
Takahashi,M.; Chiba,Y.; Ishida,S.; Murakawa,K.; Ono,Y.;
Takiguchi,S.; Watanabe,S.; Kimura,K.; Murakami,K.;
Ishii,S.; Kawai,Y.; Saito,K.; Yamamoto,J.;
Wakamatsu,A.; Nakamura,Y.; Nagahari,K.; Masuho,Y.;
Ninomiya,K.; Iwayanagi,T.

TITLE (TI): NEDO human cDNA sequencing project

JOURNAL (SO): Unpublished

REFERENCE:

AUTHOR (AU): Isogai,T.; Otsuki,T.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

FEATURES (FEAT):

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1621 tccatgaagc ccaatgtatgc gtgtacataa 1621 tccatgaagc ccaatgtatgc gtgtacataa
1681 agcaggcaag gcgagggtgcc cgctcagtc 1681 agcaggcaag gcgagggtgcc cgctcagtc
1741 ccagaccaag aaggcctgcg gcagagccga 1741 ccagaccaag aaggcctgcg gcagagccga
1801 gggtaactcac gaaaactggg ccgcgtgggtt 1801 gggtaactcac gaaaactggg ccgcgtgggtt
1861 cttcatttgc ttccatttgc ttccatttgc 1861 cttcatttgc ttccatttgc ttccatttgc
1921 tcagttatca tcacaaacat gagccaaaag 1921 tcagttatca tcacaaacat gagccaaaag
1981 cacacacaca catgcacacaca acacatacac 1981 cacacacaca catgcacacaca acacacgcac
2041 acatttgtc cacaacctca cgggacgtgg 2041 acatttgtc cacaacctca cgggacgtgg
2101 acacaaatac attttttaaa atc 2101 acacaaatac attttttaaa atc

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GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BG729430 GenBank (R)
GenBank ACC. NO. (GBN): BG729430
GenBank VERSION (VER): BG729430.1 GI:14014505
CAS REGISTRY NO. (RN): 337152-08-6
SEQUENCE LENGTH (SQL): 508
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 9 May 2001
DEFINITION (DEF): fo84d12.y1 zebrafish gridded kidney *Danio rerio* cDNA
clone 4726726 5' similar to TR:035464 035464
SEMAPHORIN ***VIA*** PRECURSOR. ;, mRNA
sequence.
SOURCE: zebrafish.
ORGANISM (ORGN): *Danio rerio*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Actinopterygii; Neopterygii; Teleostei;
Ostariophysi; Cypriniformes; Cyprinidae; *Danio*
NUCLEIC ACID COUNT (NA): 106 a 152 c 143 g 107 t
COMMENT:

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zebrafish@watson.wustl.edu

CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address: www.resgen.com
) (email contact: info@resgen.com) and
RessourcenZentrumPrimärDatenbank, Berlin, Germany (web address:
www.rzpd.de)

Seq primer: T3 ET from Amersham
High quality sequence stop: 480.

REFERENCE: 1 (bases 1 to 508)
AUTHOR (AU): Clark,M.; Johnson,S.L.; Lehrach,H.; Lee,R.; Li,F.;
Marra,M.; Eddy,S.y; Hillier,L.; Kucaba,T.; Martin,J.;
Beck,C.; Wylie,T.; Underwood,K.; Steptoe,M.;
Theising,B.; Allen,M.; Bowers,Y.; Person,B.;
Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.;
Ritter,E.; Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.;
McCann,R.; Wilson,R.
TITLE (TI): WashU Zebrafish EST Project 1998
JOURNAL (SO): Unpublished (1998)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..508	/organism="Danio rerio" /db-xref="taxon:7955" /clone="4726726" /clone-lib="zebrafish gridded kidney" /sex="mixed" /tissue-type="kidney pooled from 300 wild type adults" /lab-host="XLOR" /note="Organ: kidney; Vector: pBK-CMV; Site-1: EcoRI; Site-2: XhoI; Oligo dT cDNA library constructed from mRNA pooled from pooled kidney tissue from 300 adult zebrafish."

SEQUENCE (SEQ):

1 tttccgcgtg tggcgcgtgt gtgttaagagc gacagcggcg gctctcagcg tggctggag
61 aaacagtggaa catcttcctt gaagacgcgc ctgaactgtc ccatattctg gagactcaca
121 cttctacttc aacatccctgc aggccgtgac cgacgtcata cacatcagcg gacgagacgt
181 ggtcatggcc accttctcca caccctacaa cagtattccg ggatccgtg tggctggta
241 tgacatgtca gagatcgctc tggccttac cggacgcttc aaagaggaga aatcacctga
301 ctccacacctgg acacctgtgc cggaggagag ggtgcccgg cccaggccgg gttgtgtgc
361 cggctcgtcc tccgtggaga agtttaaagt gtcgagttag tttccggacg attctctgag
421 cttcatcaaa gcccacccgc tggatggaga ggccgtgccc gccatcgcca accggccctg
481 gttccctcaag accatggta ggtaccgg

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LOCUS (LOC): BG642108 GenBank (R)
GenBank ACC. NO. (GBN): BG642108
GenBank VERSION (VER): BG642108.1 GI:13774034
CAS REGISTRY NO. (RN): 333222-70-1
SEQUENCE LENGTH (SQL): 622
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 23 Apr 2001
DEFINITION (DEF): pg11c.pk002.g3 Chicken liver cDNA library Gallus gallus
cDNA clone pg11c.pk002.g3 5' similar to gi|9055334
ref|NP_061214.1| sema domain, transmembrane domain
(TM), and cytoplasmic domain, (***semaphorin***)
6A [Mus musculus] sp|035464|SM6A_MOUSE
SEMAPHORIN ***6A*** PRECURSOR (***SEMAPHORIN*** ***VIA***) (SEMA VIA)
(SEMAPHORIN Q) (SEMA Q) gb|AAB86408.1|, mRNA sequence.

SOURCE:
ORGANISM (ORGN):

chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Archosauria; Aves; Neognathae;
Galliformes; Phasianidae; Phasianinae; Gallus

NUCLEIC ACID COUNT (NA): 186 a 120 c 147 g 163 t 6 others

COMMENT:

Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

REFERENCE: 1 (bases 1 to 622)
AUTHOR (AU): Morgan,R.W.; Burnside,J.; Cogburn,L.A.

TITLE (TI): Chicken liver ESTs (2001)
JOURNAL (SO): Unpublished (2001)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..622	/organism="Gallus gallus" /db-xref="taxon:9031" /clone="pg11c.pk002.g3" /clone-lib="Chicken liver cDNA Library" /sex="Male and Female" /tissue-type="liver" /lab-host="E.coli EMDH10B" /note="Vector: pCMVSPORT 6"

SEQUENCE (SEQ):

1 gaggcttcct ctgctgtgcg cctctgtat gctaattgagt ctgtcccaat gccgagctgt
61 cagcttcctt gaagatgagg accctattaa cattgttgcac taccactattt caaggcaata
121 tccagttttt agaggacgccc cttcaggcaat tgaatcttag cacagactgg acttccaact
181 gatgctgaaa attcgagaca cactttatata cgctggcagg gatcaagttt acactgtaaa
241 cttaaatggaa gttccaaaat cagaagttac tccaaagcagg aaattaacat ggaggtcaag
301 gcagcaggac agagagaact gtgctatggaa agggaaaatcat aaagatgaat gccataactt
361 cattaaatgtc ttctgttccaa gaaatgacga gatgggtttt gtctgtggaa caaatgcatt
421 taatccatgt tcgagataact atcggttgcac ttcgtttagat tatgtatgggg agggaaatttag
481 tggtttggca agatgcccattt ttgtatggcag acaaaccat gtcgnnnnnn ttgtatgttgg
541 aaaattgtat tcagcaacag tagcagattt cctggcaatg gatgttgcattttatgcag
601 catggagat ggatctgccc ta

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GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BG553452 GenBank (R)
GenBank ACC. NO. (GBN): BG553452
GenBank VERSION (VER): BG553452.1 GI:13565232
CAS REGISTRY NO. (RN): 330900-90-8
SEQUENCE LENGTH (SQL): 516
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 9 Apr 2001
DEFINITION (DEF): dab84d05.y1 NICHD XGC Emb4 Xenopus laevis cDNA clone
IMAGE:4203704 5' similar to TR:035464 035464
SEMAPHORIN ***VIA*** PRECURSOR. ;, mRNA
sequence.
SOURCE: African clawed frog.
ORGANISM (ORGN): Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Amphibia; Batrachia; Anura;
Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus
NUCLEIC ACID COUNT (NA): 137 a 112 c 115 g 152 t
COMMENT:
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 386.
REFERENCE: 1 (bases 1 to 516)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..516	/organism="Xenopus laevis" /db-xref="taxon:8355" /clone="IMAGE:4203704" /clone-lib="NICHD XGC Emb4" /dev-stage="embryo, stage 31-32" /lab-host="DH10B (phage-resistant)"

/note="Organ: whole embryo;
Vector: pCMV-SPORT6; Site-1: NotI;
Site-2: SalI; Cloned
unidirectionally. Primer: oligo
dT. Average insert size 2.1 kb.
Constructed by Life Technologies.
Note: This is a *Xenopus* Gene
Collection (XGC) library."

SEQUENCE (SEQ):

1 gacccacgcg tccgactcct tagaggtaaa tgcagccaac tctcttgttt tatcttgacg
61 tccctgaacg tctgactctg gaggcctctc agtttgccta atgagggtta taaatttagcc
121 gcagtcgtga gctgctcaga actcatgtaa tagaaggcatt gtcttattaa gcacacgtga
181 acggcaggag tgattcgtga aagttatctc aaaggtcaca atcaacttgt tcctgttacc
241 ctttggcca ttgctgttat tcttgccttt gtcatgggtc cagtttttttccatc tggattatt
301 gtatactgtt tctgtgacca tcgtcaggag gatattgtat ttgtccaaag gaaggacaaa
361 gatatgagtc gttcacgcag aggcttatgt gcaagtgtga ccaaactaag tggactcttc
421 agtgacaatc agtccaaaga gtcaaaagcc gaggctatcc ttgcgcctct gatgcataat
481 gggaaaattt ctacacctaa tacaactgtctt aaaaatg

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LOCUS (LOC): AK004390 GenBank (R)
GenBank ACC. NO. (GBN): AK004390
GenBank VERSION (VER): AK004390.1 GI:12835554
CAS REGISTRY NO. (RN): 322059-94-9
SEQUENCE LENGTH (SQL): 1013
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): High-Throughput CDNA Sequencing
DATE (DATE): 3 Apr 2004
DEFINITION (DEF): Mus musculus 18-day embryo whole body cDNA, RIKEN
full-length enriched library, clone:1110067B02
product:weakly similar to ***SEMAPHORIN***
6A PRECURSOR (***SEMAPHORIN*** ***VIA***
) (SEMA VIA) (SEMAPHORIN Q) (SEMA Q) [Mus musculus],
full insert sequence.
KEYWORDS (ST): HTC; CAP trapper
SOURCE: Mus musculus (house mouse)
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

COMMENT:

Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAAGGATCCAAGAGCTCAATTAAATTAAACCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

REFERENCE: 1

AUTHOR (AU): Carninci,P.; Hayashizaki,Y.
TITLE (TI): High-efficiency full-length cDNA cloning
JOURNAL (SO): Meth. Enzymol., 303, 19-44 (1999)
OTHER SOURCE (OS): CA 131:318304

REFERENCE: 2

AUTHOR (AU): Carninci,P.; Shibata,Y.; Hayatsu,N.; Sugahara,Y.;
Shibata,K.; Itoh,M.; Konno,H.; Okazaki,Y.;
Muramatsu,M.; Hayashizaki,Y.
TITLE (TI): Normalization and subtraction of cap-trapper-selected
cDNAs to prepare full-length cDNA libraries for rapid
discovery of new genes
JOURNAL (SO): Genome Res., 10 (10), 1617-1630 (2000)
OTHER SOURCE (OS): CA 134:305920

REFERENCE: 3

AUTHOR (AU): Shibata,K.; Itoh,M.; Aizawa,K.; Nagaoka,S.; Sasaki,N.;
Carninci,P.; Konno,H.; Akiyama,J.; Nishi,K.;
Kitsunai,T.; Tashiro,H.; Itoh,M.; Sumi,N.; Ishii,Y.;
Nakamura,S.; Hazama,M.; Nishine,T.; Harada,A.;

Yamamoto,R.; Matsumoto,H.; Sakaguchi,S.; Ikegami,T.;
Kashiwagi,K.; Fujiwake,S.; Inoue,K.; Togawa,Y.;
Izawa,M.; Ohara,E.; Watahiki,M.; Yoneda,Y.;
Ishikawa,T.; Ozawa,K.; Tanaka,T.; Matsuura,S.;
Kawai,J.; Okazaki,Y.; Muramatsu,M.; Inoue,Y.; Kira,A.;
Hayashizaki,Y.

TITLE (TI): RIKEN integrated sequence analysis (RISA)
system--384-format sequencing pipeline with 384
multicapillary sequencer

JOURNAL (SO): Genome Res., 10 (11), 1757-1771 (2000)

OTHER SOURCE (OS): CA 134:203311

4

REFERENCE: AUTHOR (AU): The RIKEN Genome Exploration Research Group Phase II
Team; the FANTOM Consortium.

TITLE (TI): Functional annotation of a full-length mouse cDNA
collection

JOURNAL (SO): Nature, 409, 685-690 (2001)

OTHER SOURCE (OS): CA 134:203311

5

REFERENCE: AUTHOR (AU): The FANTOM Consortium; the RIKEN Genome Exploration
Research Group Phase I & II Team.

TITLE (TI): Analysis of the mouse transcriptome based on functional
annotation of 60,770 full-length cDNAs

JOURNAL (SO): Nature, 420, 563-573 (2002)

OTHER SOURCE (OS): CA 138:131939

REFERENCE: AUTHOR (AU): 6 (bases 1 to 1013)

Adachi,J.; Aizawa,K.; Akahira,S.; Akimura,T.; Arai,A.;
Aono,H.; Arakawa,T.; Bono,H.; Carninci,P.; Fukuda,S.;
Fukunishi,Y.; Furuno,M.; Hanagaki,T.; Hara,A.;
Hayatsu,N.; Hiramoto,K.; Hiraoka,T.; Hori,F.;
Imotani,K.; Ishii,Y.; Itoh,M.; Izawa,M.; Kasukawa,T.;
Kato,H.; Kawai,J.; Kojima,Y.; Konno,H.; Kouda,M.;
Koya,S.; Kurihara,C.; Matsuyama,T.; Miyazaki,A.;
Nishi,K.; Nomura,K.; Numazaki,R.; Ohno,M.; Okazaki,Y.;
Okido,T.; Owa,C.; Saito,H.; Saito,R.; Sakai,C.;
Sakai,K.; Sano,H.; Sasaki,D.; Shibata,K.; shibata,Y.;
Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Suzuki,H.;
Tagami,M.; Tagawa,A.; Takahashi,F.; Tanaka,T.;
Tejima,Y.; Toya,T.; Yamamura,T.; Yasunishi,A.;
Yoshida,K.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (10-JUL-2000) Yoshihide Hayashizaki, The
Institute of Physical and Chemical Research (RIKEN),
Laboratory for Genome Exploration Research Group, RIKEN
Genomic Sciences Center (GSC), RIKEN Yokohama
Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-
res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>,
Tel:81-45-503-9222, Fax:81-45-503-9216)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1013	/organism="Mus musculus" /mol-type="mRNA" /strain="C57BL/6J" /db-xref="FANTOM-DB:1110067B02" /db-xref="taxon:10090" /clone="1110067B02" /tissue-type="whole body" /clone-lib="RIKEN full-length enriched mouse cDNA library" /dev-stage="18-day embryo" /note="weakly similar to SEMAPHORIN 6A PRECURSOR (SEMAPHORIN VIA) (SEMA VIA) (SEMAPHORIN Q) (SEMA Q) [Mus musculus] (SWISSPROT 035464, evidence: FASTY, 60.6%ID, 64.8%length, match=1719)"
misc-feature	1..1013	

SEQUENCE (SEQ):

1 gcagccagca cctgaggact tcttatacag tcataaagcc accttagagcg atttgggtt
61 gagcaacccg ccccttccct ccaggatcg aagcacacca cccttgccat gataaacatt
121 ccatcccctg ctgttctgat aatgtgaagt cagatgaggg ttcccgagggtt atgtggcacc
181 tgcggaaacc atgtcttagag tcgtttctat gtagcttgcg agagccact gatggctgca

241 ggtgtgttagc ctactgacag ctttggttaa cccactgcac atcaccagg catttaccca
 301 acttactcta gaaatgtcca cagctaagga aggctctga gccagtcagg cggagttcaa
 361 gtgatatctt gggacagtga ccatggctcg cattactgg gggaggatgg ggtacaagac
 421 accagatcat tttatacag gatgttagt actgtgcgg ttgatcttt ccttcaagaa
 481 cattctttc tatagaaaaa tgattccctg tgatctctg gaagctccaa agctgaaacc
 541 cttcagcttt gcaactaaaa atattacagt ttaataatca attaaaccaa ccaacaataa
 601 gcaactacaca tctgccacca acaatgttg ttgcattac cttaccaata ttaatccag
 661 cgtgtaact ctgtgtgacc ccgataacat ttgttaacat tggctgcct tagagttgt
 721 actgtgagtt ctatcgtat ttatgttcaa atttctaaca tggattctag tctctattct
 781 gttaaattaa ttttaaatgc tttatccatt tggcaaaagg taaacacaga ttgtatctt
 841 tttaaatggta cggataaaaa aaataaccct aaagtgaagt ggctctatac tggatgttaa
 901 agtactttaa cgtgtataga tatcttggta acttgtattt tggatgttaa aataatatgt
 961 acttgggtt tttacacccg catgtaaagt caaaataaaa tatccaagtc att

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LOCUS (LOC): AF288666 GenBank (R)
GenBank ACC. NO. (GBN): AF288666
GenBank VERSION (VER): AF288666.1 GI:11093908
CAS REGISTRY NO. (RN): 301990-09-0
SEQUENCE LENGTH (SQL): 3018
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Rodents
DATE (DATE): 11 Dec 2000
DEFINITION (DEF): *Mus musculus* axon guidance signal SEMA6A1 mRNA, complete cds.
SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus* Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Mus*
NUCLEIC ACID COUNT (NA): 774 a 859 c 744 g 641 t
REFERENCE:
AUTHOR (AU): Klostermann,A.; Lutz,B.; Gertler,F.; Behl,C.
TITLE (TI): The orthologous human and murine ***semaphorin***
 6A - ***1*** proteins (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated phosphoprotein-like protein (EVL) via a novel carboxyl-terminal zyxin-like domain
JOURNAL (SO): J. Biol. Chem., 275 (50), 39647-39653 (2000)
OTHER SOURCE (OS): CA 134:189679
REFERENCE:
AUTHOR (AU): Klostermann,A.; Behl,C.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (21-JUL-2000) Independent Research Group Neurodegeneration, MPI of Psychiatry, Kraepelinstrasse 2-10, Munich 80804, Germany

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..3018	/organism="Mus musculus" /db-xref="taxon:10090" /tissue-type="brain" /codon-start=1 /product="axon guidance signal SEMA6A1" /protein-id="AAG29494.1" /db-xref="GI:11093909" /translation="MRPAALLCLTLLCAGAGF PEDSEPISHGNYTKQYPFVGH KPGRNTTQRHRLDIQMIMMNRTLHYAARDHIYT VDIDTSHTEEIYCSKKLTWKSRA DVDTCRMKGKHKDECHNFIVKLKNNDDTLFVCG TNAFPNSCRNYRVDTLETFGDEFS GMARCPYDAKHVNIALFADGKLYSATVTDFAID AVIYRSPGDSPTLRTVKHDSKWLK EPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSF LKARLNCSVPGDSHFYFNILQAVTDVIRINGRDV VLATFSTPYNSIPGSAVCAYDMLD IADVFTGRFKEQKSPDSTWTPVDERVPKPRPGC CAGSSSLEYKATSNEFPDDTLNFI KTHPLMDEAVPSIINRPWFLRTMRYRLTKIAVD NAAGPYQNHTVVFLEEMNVYNPEK CSYDGVEDKRIMGMQLDRASGLYVAFSTCVIKV"
CDS	1..3018	

PLGRCERHGKCKTCIASRDPYCG
 WVRESGSCHAHLSPLSLRTFEQDIERGNTDGLGDC
 HNSFVALNHGSSLYPNTTSDSA
 SRDGYESRGMLDWNDLLEAPGSTDPLGAVSSH
 HQDKKGVIRESYLKNSDQLVPVTL
 LAIAVILAFAVFMGAVFSGIIVYCVCDHRRKDVAVV
 RRKEKELTHSRRGSMSSVSELGL
 FGDTQSNDPKPEAILTPLMHNGKLATSSNTAKML
 IKADQHHLTLALPTPESTPTLQQ
 KRKPNRGSREWERNQNIINACTKDMPPMGSPVIP
 TDLPLRASPCHIPSVVLPITQOG
 YQHEYVVDQPKMSEVVAQMALEDQAATLEYKTTKE
 HLSSKSPNHGVNLVENLDSLPPKV
 PQREASLGPPGTSLSQTGLSKRLEMHQHSSSYGLE
 YKRSYPTNSLTRSHQTTTLKRNN
 NSSNSHLSRNQSFGRGDNPPPAPQRVDSIQVHS
 SQPSGQAVTVSRQPSLNAYNSLTR
 SGLKRTPSLKPVDPPKPSFAPLSTSMKPNDACT"

SEQUENCE (SEQ):

1 atgcggccag	cagccttact	gctgtgtctc	acactgtctac	actgcgccgg	ggcggtttc
61 ccagaagatt	ccgagccat	cagtatttcg	catggcaact	atacaaaaca	gtatccggtg
121 tttgtggcc	acaagccagg	acgaaacacc	acgcagaggc	acaggctgga	catccagatg
181 atcatgtatca	tgaacagaac	cctctacgtt	gctgctcgag	accatattta	tactgttgat
241 atagacacat	cccacacaga	agaaaattac	tgttagaaaa	aactgacatg	gaaatctaga
301 caggctgacg	tagacacatg	caggatgaag	ggggaaacata	aggatgaatg	tcacaacttc
361 attaaagttc	ttctcaagaa	gaatgatgat	acgcttgg	tctgtggaa	caatgccttc
421 aacccttcct	gcagaaacta	cagggtcgat	accttggaaa	cttttgggaa	tgaattttagc
481 ggaatggcca	gatgcccta	tgatgccaaa	catgtcaaca	tcgtctgtt	tgcagatgga
541 aaactctact	cggctacagt	gactgacttt	ctggccattt	atgcggatcat	ttacaggagc
601 cccggagaca	gccctaccc	caggactgtc	aagcatgatt	caaagtgggt	gaaagagccg
661 tactttgtcc	aagccgtgga	ttatggggac	tatatactact	tcttcttcag	agaaatttgca
721 gtagaataca	acactatggg	aaagggttgg	ttcccttaggg	tggctcagg	ctgtaaagat
781 gacatggggag	ggtctcagag	agtccctggag	aaggcgttgg	catcttcc	gaaggctcgc
841 ctgaactgct	cggtgcctgg	agactctcat	ttttatttca	atatactcca	ggcagttaca
901 gatgtgattc	gcattaaatgg	ccgtatgtt	gtcttggca	cctttccac	accttataac
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GenBank VERSION (VER): AF279656.1 GI:11093650
 CAS REGISTRY NO. (RN): 386088-74-0
 SEQUENCE LENGTH (SQL): 3862
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 11 Dec 2000
 DEFINITION (DEF): Homo sapiens semaphorin SEMA6A1 mRNA, complete cds.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 971 a 1111 c 967 g 813 t
 REFERENCE:
 AUTHOR (AU): Klostermann,A.; Lutz,B.; Gertler,F.; Behl,C.
 TITLE (TI): The orthologous human and murine ***semaphorin***
 6A - ***1*** proteins (SEMA6A-1/Sema6A-1)
 bind to the enabled/vasodilator-stimulated
 phosphoprotein-like protein (EVL) via a novel
 carboxyl-terminal zyxin-like domain
 JOURNAL (SO): J. Biol. Chem., 275 (50), 39647-39653 (2000)
 OTHER SOURCE (OS): CA 134:189679
 REFERENCE:
 AUTHOR (AU): Klostermann,A.; Lutz,B.; Gertler,F.; Behl,C.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (19-JUN-2000) Independent Research Group
 Neurodegeneration, MPI of Psychiatry, Kraepelinstrasse
 2-10, Munich 80804, Germany

FEATURES (FEAT):		Location	Qualifier
source	1..3862		/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="5" /map="5q21-22"
CDS	658..3750		/note="guidance signal" /codon-start=1 /product="semaphorin SEMA6A1" /protein-id="AAG29378.1" /db-xref="GI:11093651" /translation="MRSEALLLYFTLLHFAGAGF PEDSEPISHGNYTKQYPVFVGH KPGRNTTQRHRLDIQMIMIMNGTLTYIAARDHIYT VDIDTSHTEEIYCSKKLTWKSRQA DVTDCRMKGKHDECHNFIVKLKNNDALFVCG TNAFPNSCRNYKMDTLEPGFDEFS GMARCPYDAKHNVALFADGKLYSATVTDFLAID AVIYRSLGESPTLRTVKHDSKWLK EPYFVQAVDYGDIYFFFREIAVEYNTMGKVWFP RVAQVCKNDMGGSQRVLEKQWTSF LKARLNCSVPGDSHFYFNILQAVTDVIRINGRDV VLATFSTPYNSIPGSACVAYDMLD IASVFTGRFKEQKSPDSTWTPVDERVPKPRPGC CAGSSSLERYATSNEFPPDDTLNFI KTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVD TAAGPYQNHTVVFLGSEKGIIILKF LARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVED KRIMGMQLDRASSSLYVAFSTCVI KVPLGRCRERHGKCKKTCIASRDPYCGWIKEGGAC SHLSPNSRLTFFEQDIERGNTDGLG DCHNSFVALNGHSSSLPSTTSYSTAQEGYESR GGMLDWKHLLDSDPSTDPLGAVSS HNHQDKKGVIRESYLYKGHDQLVPVTLLAIAVILA FVMGAVFSGITVYCVCDHRRKDVA VVQRKEKELHSRRGSMSSVTKLSSGLFGDTQSKD PKPEAILTPLMHNGKLATPGNTAK MLIKADQHHLDLTALPTPESTPTLQQKRKPSRGS REWERNQNLIINACTKDMPPMGSBV IPTDLPLRASPISHPSVVLPITQQGYQHEYVDQ PKMSEVAQMALEDQAATLEYKTIK EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGP PGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNNNTNSSNSHLS RNQSFGRGDNPAPQRVDSIQVH SSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSL

SEQUENCE (SEQ):

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MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 29 Dec 2000
DEFINITION (DEF): uy22c05.y1 NCI_CGAP_Lu30 Mus musculus cDNA clone
IMAGE:3660296 5' similar to TR:035464 035464
SEMAPHORIN ***VIA*** PRECURSOR. ;, mRNA
sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 117 a 90 c 97 g 99 t

COMMENT:
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1421064
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.

REFERENCE:
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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SEQUENCE (SEQ):

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L4 ANSWER 71 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AK021660 GenBank (R)
GenBank ACC. NO. (GBN): AK021660
GenBank VERSION (VER): AK021660.1 GI:10432889
CAS REGISTRY NO. (RN): 390309-92-9
SEQUENCE LENGTH (SQL): 1588
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 30 Jan 2004
DEFINITION (DEF): Homo sapiens cDNA FLJ11598 fis, clone HEMBA1003866,
moderately similar to Mus musculus ***semaphorin***
VIA mRNA.

KEYWORDS (ST): oligo capping; fis (full insert sequence)

SOURCE: Homo sapiens (human)

ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

COMMENT: NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

REFERENCE: 1

AUTHOR (AU): Ota,T.; Suzuki,Y.; Nishikawa,T.; Otsuki,T.;
Sugiyama,T.; Irie,R.; Wakamatsu,A.; Hayashi,K.;
Sato,H.; Nagai,K.; Kimura,K.; Makita,H.; Sekine,M.;
Obayashi,M.; Nishi,T.; Shibahara,T.; Tanaka,T.;
Ishii,S.; Yamamoto,J.; Saito,K.; Kawai,Y.; Isono,Y.;
Nakamura,Y.; Nagahari,K.; Murakami,K.; Yasuda,T.;
Iwayanagi,T.; Wagatsuma,M.; Shiratori,A.; Sudo,H.;
Hosoiri,T.; Kaku,Y.; Kodaira,H.; Kondo,H.; Sugawara,M.;
Takahashi,M.; Kanda,K.; Yokoi,T.; Furuya,T.;
Kikkawa,E.; Omura,Y.; Abe,K.; Kamihara,K.; Katsuta,N.;
Sato,K.; Tanikawa,M.; Yamazaki,M.; Ninomiya,K.;
Ishibashi,T.; Yamashita,H.; Murakawa,K.; Fujimori,K.;
Tanai,H.; Kimata,M.; Watanabe,M.; Hiraoka,S.; Chiba,Y.;
Ishida,S.; Ono,Y.; Takiguchi,S.; Watanabe,S.;
Yosida,M.; Hotuta,T.; Kusano,J.; Kanehori,K.;
Takahashi-Fujii,A.; Hara,H.; Tanase,T.; Nomura,Y.;
Togoya,S.; Komai,F.; Hara,R.; Takeuchi,K.; Arita,M.;
Imose,N.; Musashino,K.; Yuuki,H.; Oshima,A.; Sasaki,N.;
Aotsuka,S.; Yoshikawa,Y.; Matsunawa,H.; Ichihara,T.;
Shiohata,N.; Sano,S.; Moriya,S.; Momiyama,H.; Satoh,N.;
Takami,S.; Terashima,Y.; Suzuki,O.; Nakagawa,S.;
Senoh,A.; Mizoguchi,H.; Goto,Y.; Shimizu,F.; Wakebe,H.;
Hishigaki,H.; Watanabe,T.; Sugiyama,A.; Takemoto,M.;
Kawakami,B.; Yamazaki,M.; Watanabe,K.; Kumagai,A.;
Itakura,S.; Fukuzumi,Y.; Fujimori,Y.; Komiya,M.;
Tashiro,H.; Tanigami,A.; Fujiwara,T.; Ono,T.;
Yamada,K.; Fujii,Y.; Ozaki,K.; Hirao,M.; Ohmori,Y.;
Kawabata,A.; Hikiji,T.; Kobatake,N.; Inagaki,H.;
Ikeda,Y.; Okamoto,S.; Okitani,R.; Kawakami,T.;
Noguchi,S.; Itoh,T.; Shigeta,K.; Senba,T.;
Matsumura,K.; Nakajima,Y.; Mizuno,T.; Morinaga,M.;
Sasaki,M.; Togashi,T.; Oyama,M.; Hata,H.; Watanabe,M.;
Komatsu,T.; Mizushima-Sugano,J.; Satoh,T.; Shirai,Y.;
Takahashi,Y.; Nakagawa,K.; Okumura,K.; Nagase,T.;
Nomura,N.; Kikuchi,H.; Masuho,Y.; Yamashita,R.;
Nakai,K.; Yada,T.; Nakamura,Y.; Ohara,O.; Isogai,T.;
Sugano,S.

TITLE (TI): Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL (SO): Nat. Genet., 36 (1), 40-45 (2004)

OTHER SOURCE (OS): CA 140:158332

REFERENCE: 2

AUTHOR (AU): Isogai,T.; Ota,T.; Hayashi,K.; Sugiyama,T.; Otsuki,T.;
Suzuki,Y.; Nishikawa,T.; Nagai,K.; Sugano,S.;
Shiratori,A.; Sudo,H.; Wagatsuma,M.; Hosoiri,T.;
Kaku,Y.; Kodaira,H.; Kondo,H.; Sugawara,M.;
Takahashi,M.; Chiba,Y.; Ishida,S.; Murakawa,K.; Ono,Y.;
Takiguchi,S.; Watanabe,S.; Kimura,K.; Murakami,K.;
Ishii,S.; Kawai,Y.; Saito,K.; Yamamoto,J.;
Wakamatsu,A.; Nakamura,Y.; Nagahari,K.; Masuho,Y.;
Ninomiya,K.; Iwayanagi,T.

TITLE (TI): NEDO human cDNA sequencing project

JOURNAL (SO): Unpublished

REFERENCE: 3 (bases 1 to 1588)

AUTHOR (AU): Isogai,T.; Otsuki,T.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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CDS	65..1168	

SEQUENCE (SEQ):

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 601 agattcggtt ttctacttttgc atgttctgca gtctattaca gacataatac aaatcaatgg
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L4 ANSWER 72 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AX026746 GenBank (R)

GenBank ACC. NO. (GBN): AX026746

GenBank VERSION (VER): AX026746.1 GI:10187890

CAS REGISTRY NO. (RN): 386088-75-1

SEQUENCE LENGTH (SQL): 3862

MOLECULE TYPE (CI): DNA; linear

DIVISION CODE (CI): Patent

DATE (DATE): 16 Sep 2000

DEFINITION (DEF): Sequence 6 from Patent WO0031252.

SOURCE: human.

ORGANISM (ORGN): Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 971 a 1111 c 967 g 813 t

REFERENCE:
 AUTHOR (AU): Klostermann,A.; Behl,C.
 TITLE (TI): Human ***semaphorin*** ***6a*** - ***1***
 (sema6a-a), a gene involved in neuronal development and
 regeneration mechanisms during apoptosis, and its use
 as a potential drug target
 JOURNAL (SO): Patent: WO 0031252-A 6 02-JUN-2000; KLOSTERMANN ANDREAS
 (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL CHRISTIAN
 (DE)

FEATURES (FEAT):

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SEQUENCE (SEQ):

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 601 ccgtcgatgc accgaaaagg gtgaagttaga gaaataaagt 1
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 3781 agcaggcaag gcgagggtgcc cgctcagtc agcaagggttc tcaactgcct cgagtaccca
 3841 ccagaccaag aaggcctgcgc gc

L4 ANSWER 73 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AX026743 GenBank (R)
GenBank ACC. NO. (GBN): AX026743
GenBank VERSION (VER): AX026743.1 GI:10187888
CAS REGISTRY NO. (RN): 390282-37-8
SEQUENCE LENGTH (SQL): 216
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Patent
DATE (DATE): 16 Sep 2000
DEFINITION (DEF): Sequence 3 from Patent WO0031252.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
NUCLEIC ACID COUNT (NA): 45 a 85 c 51 g 35 t
REFERENCE:
AUTHOR (AU): Klostermann,A.; Behl,C.
TITLE (TI): Human ***semaphorin*** ***6a*** - ***1***
 (semaphorin-6a), a gene involved in neuronal development and
 regeneration mechanisms during apoptosis, and its use
 as a potential drug target
JOURNAL (SO): Patent: WO 0031252-A 3 02-JUN-2000; KLOSTERMANN ANDREAS
 (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL CHRISTIAN
 (DE)
FEATURES (FEAT):
 Feature Key Location Qualifier

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L4 ANSWER 74 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AX026741 GenBank (R)
GenBank ACC. NO. (GBN): AX026741
GenBank VERSION (VER): AX026741.1 GI:10187886
CAS REGISTRY NO. (RN): 390282-36-7
SEQUENCE LENGTH (SQL): 3093
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Patent
DATE (DATE): 16 Sep 2000
DEFINITION (DEF): Sequence 1 from Patent WO0031252.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 813 a 855 c 765 g 660 t
REFERENCE:
 1 (bases 1 to 3093)
 AUTHOR (AU): Klostermann,A.; Behl,C.
 TITLE (TI): Human ***semaphorin*** - ***1***
 (semaphorin-a), a gene involved in neuronal development and
 regeneration mechanisms during apoptosis, and its use
 as a potential drug target
 JOURNAL (SO): Patent: WO 0031252-A 1 02-JUN-2000; KLOSTERMANN ANDREAS
 (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL CHRISTIAN
 (DE)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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SEQUENCE (SEQ):

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LOCUS (LOC): AW343314 GenBank (R)
 GenBank ACC. NO. (GBN): AW343314
 GenBank VERSION (VER): AW343314.1 GI:6839680
 CAS REGISTRY NO. (RN): 254706-97-3
 SEQUENCE LENGTH (SQL): 664
 MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 31 Jan 2000
DEFINITION (DEF): fi76a10.y1 Sugano Kawakami zebrafish DRA Danio rerio
cDNA clone 2643546 5' similar to TR:035464 035464
SEMAPHORIN ***VIA*** . ;, mRNA sequence.
SOURCE: zebrafish.
ORGANISM (ORGN): Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Actinopterygii; Neopterygii; Teleostei;
Ostariophysi; Cypriniformes ; Cyprinidae; Danio
NUCLEIC ACID COUNT (NA): 168 a 148 c 177 g 171 t
COMMENT:
Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center
Seq primer: T3 ET from Amersham
High quality sequence stop: 478.
REFERENCE: 1 (bases 1 to 664)
AUTHOR (AU): Sugano,S.; Kawakami,K.; Johnson,S.; Li,F.; Marra,M.;
Eddy,S.; Hillier,L.; Clifton,S.; Allen,M.; Gibbons,M.;
Jost,S.; Kucaba,T.; Martin,J.; Pape,D.; Steptoe,M.;
Underwood,K.; Theising,B.; Ritter,E. ; Bowers,Y.;
Wylie,T.; Waterston,R.; Wilson,R.
TITLE (TI): WashU Zebrafish EST Project 1999
JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..664	<pre> /organism="Danio rerio" /strain="AB" /db-xref="taxon:7955" /clone="2643546" /clone-lib="Sugano Kawakami zebrafish DRA" /sex="mixed (one male and one female, including unfertilized eggs)" /dev-stage="adult" /lab-host="DH10B (phage resistant)" /note="Vector: pME18S-FL3; Site-1: DraIII (CACTGTGTG); Site-2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA. " </pre>

SEQUENCE (SEQ):

```
 1 tctaaagaaa acacggaaaa tatggaataa gatggtgttc gaagccaaac ggttgacgga
 61 aagaacatgg tgggtctcg tcatcatggc gatgggtctta ttagcctggc tcctccact
121 cattacttct gccacgcctt ttccctagaga tctgcagcca attagtgtgg tgggatttgg
181 cgactcgtac ctgtacccca gtttcaggg tctgggtgtcc agcaatgaga cggagcgtct
241 gggctctggac tatcagcgca tgatgaggat ccagcacatg ctgtacatcg ccgcccagaga
301 ccatgtgttt gttgttaatc tcacaacccqcc aqtagatqaa attattccac aqcaqatcc
```

361 gacgtggaga tccacagacg tgtccaagtg caccgtcaga ggaagaaaaca gtgatgaatg
421 ttacaattat atcaagggttc ttgttcctcg taatgacggg actctgtttg cctgtggAAC
481 aaacgcgttg aatcctgcct gcccaacta cagattgagt tcactggagc aggtcgac
541 ggagctcttg ggtcaggcaa gatgtccatt tgagtctcga cagtc当地atg gtagagtgtt
601 tgcagggtggg tatttctatt cagccacagt gacggactta caggctagtg atgctgagat
661 ctac

L4 ANSWER 76 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AW280824 GenBank (R)
GenBank ACC. NO. (GBN): AW280824
GenBank VERSION (VER): AW280824.1 GI:6669373
CAS REGISTRY NO. (RN): 252531-29-6
SEQUENCE LENGTH (SQL): 656
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 26 Jul 2002
DEFINITION (DEF): fj46c12.y1 zebrafish adult brain *Danio rerio* cDNA 5'
similar to TR:035464 035464 ***SEMAPHORIN***
VIA . ;, mRNA sequence.
SOURCE: *Danio rerio*.
ORGANISM (ORGN): *Danio rerio*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Actinopterygii; Neopterygii; Teleostei;
Ostariophysi; Cypriniformes ; Cyprinidae; *Danio*
NUCLEIC ACID COUNT (NA): 170 a 162 c 188 g 136 t
COMMENT:
Other_ESTs: fj46c12.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zebrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimärDatenbank, Berlin, Germany (web address:
www.rzpd.de)
Seq primer: T7
High quality sequence stop: 481.
REFERENCE: 1 (bases 1 to 656)
AUTHOR (AU): Clark,M.; Johnson,S.L.; Lehrach,H.; Lee,R.; Li,F.;
Marra,M.; Eddy,S.y; Hillier,L.; Kucaba,T.; Martin,J.;
Beck,C.; Wylie,T.; Underwood,K. ; Steptoe,M.;
Theising,B.; Allen,M.; Bowers,Y.; Person,B.;
Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.;
Ritter,E.; Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.;
McCann,R.; Wilson,R.
TITLE (TI): WashU Zebrafish EST Project 1998
JOURNAL (SO): Unpublished (1998)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..656	/organism="Danio rerio" /db-xref="taxon:7955" /clone-lib="zebrafish adult brain" /sex="mixed male and female" /tissue-type="brain" /dev-stage="adult" /lab-host="E. coli DH10B" /note="Vector: pZIPLOX; Site-1: NotI; Site-2: SalI; Original library was constructed in lambdaZIPLOX. Mass excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

SEQUENCE (SEQ):
1 ctgctcggt gtgtggagct gaatgagcgc gcattgttcc tttgggtt ttcctctac

61 ccgcgcggat cgatcgatca gtgatcgatcgatgtatcgatggatataatcg
 121 atgtgaggaa ggtgtcaaac acagcggctg aagttcagaa gagatcgtgc gggacagtaa
 181 agatgcgagc gcaggccctg ctgcgttacc tgacgctgtgc gtagacggct ggagccgctt
 241 tcccaagaaga caccgagccc atcagcatcg cacatggaaa ccacactaaa cagatccac
 301 tgttcgatggg acacaaacca ggcaggaata acacacagcg acacaaactg gacatccac
 361 tgatcgatcat catgaacccgg acgctgtatg tggctgcgag ggatcacatt tacacgctgg
 421 acatggagac gtccagcaca gaggagatct tcttcgttgcgaa gaaatgtgacc tgaaatgtc
 481 gacaggcggta tggtggacacg tgcaggatga agggcaaca caagacgag tgctataact
 541 tcataaagggt gctcctgcgag cagagtggg actctctgtt tttgtgcggg accaaccgc
 601 tcaacccgtt ctgcaaaacc tacaggatgg acatgtcgatccctctgggt gaagaa

L4 ANSWER 77 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AW128036 GenBank (R)
 GenBank ACC. NO. (GBN): AW128036
 GenBank VERSION (VER): AW128036.1 GI:6115940
 CAS REGISTRY NO. (RN): 245383-36-2
 SEQUENCE LENGTH (SQL): 802
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 25 Oct 1999
 DEFINITION (DEF): fi06a12.y1 Sugano Kawakami zebrafish DRA Danio rerio
 cDNA clone 2600350 5' similar to TR:035464 035464
 SEMAPHORIN ***VIA*** . ;, mRNA sequence.
 SOURCE: zebrafish.
 ORGANISM (ORGN): Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Actinopterygii; Neopterygii; Teleostei;
 Ostariophysi; Cypriniformes ; Cyprinidae; Danio
 NUCLEIC ACID COUNT (NA): 202 a 182 c 212 g 202 t 4 others
 COMMENT:
 Other_ESTs: fi06a12.x1
 Contact: S.L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
 Sequencing by: Washington University Genome Sequencing Center
 Seq primer: T3 ET from Amersham
 High quality sequence stop: 488.
 REFERENCE: 1 (bases 1 to 802)
 AUTHOR (AU): Sugano,S.; Kawakami,K.; Johnson,S.; Li,F.; Marra,M.;
 Eddy,S.; Hillier,L.; Clifton,S.; Allen,M.; Gibbons,M.;
 Jost,S.; Kucaba,T.; Martin,J.; Pape,D.; Steptoe,M.;
 Underwood,K.; Theising,B.; Ritter,E. ; Bowers,Y.;
 Wylie,T.; Waterston,R.; Wilson,R.
 TITLE (TI): WashU Zebrafish EST Project 1999
 JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..802	/organism="Danio rerio" /strain="AB" /db-xref="taxon:7955" /clone="2600350" /clone-lib="Sugano Kawakami zebrafish DRA" /sex="mixed (one male and one female, including unfertilized eggs)" /dev-stage="adult" /lab-host="DH10B (phage resistant)" /note="Vector: pME18S-FL3; Site-1: DraIII (CACTGTGTG); Site-2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site

CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA. "

SEQUENCE (SEQ):

```

1 tttaaagaaa acacggaaa tatgaaataa gatgggttgc gaagccaaac ggttgcgg
61 aagaacatgg tggctctg tcatcatggc gatggctta ttagcctggc tcctccact
121 cattacttct gccacgcctt ttccttagaga tctgcagcca attagtgtgg tgggattgga
181 cgactcgatc ctgtacccca gtttcaggg tctgggttcc agcaatgaga cggagcgtct
241 gggctctggac tatcagcgca tggatgaggat ccagcacatg ctgtacatcg ccgcccagaga
301 ccatgtgttt gttgttaatc tcacaacggc agtagatgaa attattccac agcagatcct
361 gacgtggaga tccacagacg tggccaaatg caccgtcaga ggaagaaaca gtgatgaatg
421 ttacaattat atcaagggtt ttgtccctcg taatgacgag actctgtttg cctgtggAAC
481 aaacgcgttg aatcctgcctt ggcgcacta cagattgatg tcaactggagc aggtcgagaca
541 ggagctttt ggtcaggcaa gatgtccatt tgagtctcgatcagtgatc tangagtgtg
601 tgcacgtgtt catttctatt cagccacagt gacggacttc caggcagatg atgctgtgat
661 ctacaggat ntangagag aggccgacc tggctgcgc actgtcaat accactgcaa
721 atggctcana gagcctcatt ccctgcacgc tggcaatac cggaaactat ggtatttctt
781 ctccaaatgaa aatgctgatg ag

```

L4 ANSWER 78 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI800602 GenBank (R)
 GenBank ACC. NO. (GBN): AI800602
 GenBank VERSION (VER): AI800602.1 GI:5366162
 CAS REGISTRY NO. (RN): 238193-66-3
 SEQUENCE LENGTH (SQL): 820
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 19 Dec 1999
 DEFINITION (DEF): wg12d10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens
 cDNA clone IMAGE:2364883 3' similar to TR:035464 035464
 SEMAPHORIN ***VIA*** . ;, mRNA sequence.

SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 208 a 170 c 157 g 279 t 6 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1688 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 447.

REFERENCE: 1 (bases 1 to 820)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..820	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2364883" /clone-lib="Soares-NSF-F8-9W-OT-PA-P-S1" /lab-host="DH10B" /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Equal amounts of plasmid DNA from five

normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

SEQUENCE (SEQ):

1 ttttaatatt ttacagtca gttttattac ttttaagtaa taaagagcct tttccttgct
61 tttctttttt ccctttttt cttttctttt ttcttttctt acaacataca ttaagtcgtg
121 aatcagatgt taggggatgt ggagatggaa ggaaaatgg tgacatcaca atattttac
181 aactttacaa caaatataaa tctgagttt tgcatctac cagtgtctag caaggggtgga
241 aagcaaaggc acactcgggt ttatggaccc tacccatata attcttacaa acctgagcca
301 ctcttggaa aactaccc ttccatgggtgt tataactccac tgctatttcc ctgaagaaga
361 agtagatata atctccgtaa tccacggctt gaacaaagta tgggttcttcc aaccattttg
421 aatcgtgctt gacggtccgc agggtagggc tttctccaag actccggtaa atgactgcgt
481 caatggcaag gaagtcaagc actgtggctg agtatagttn tccatctngc aacagtgcaa
541 cgttggcatg tttggcatca tatgggcattc tggccattcc actgaattca tccccgaatg
601 ttncaatgtta tccatcttta tagttctgca ggaagggtt angggcatag ttccacagac
661 caacaatgca tcatccgtt tctttagaag aactttann taagtgtggc aactcatccc
721 tatgtttcc cttcattctg catgtggcta ccatcggct gtctaagatt tcccatgcag
781 ttttttgc acataaaatt tctttccggg gtgatgtt

L4 ANSWER 79 OF 86 GENBANK.RTM. COPYRIGHT 2004 ON STN

LOCUS (LOC): AI571889 GenBank (R)
GenBank ACC. NO. (GBN): AI571889
GenBank VERSION (VER): AI571889.1 GI:4535263
CAS REGISTRY NO. (RN): 229599-17-1
SEQUENCE LENGTH (SQL): 414
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 12 May 1999
DEFINITION (DEF): to20g10.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone
IMAGE:2179650 3' similar to TR:035464 035464
SEMAPHORIN ***VIA*** . ;, mRNA sequence.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 94 a 86 c 89 g 145 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 978 Std Error: 0.00
Seq primer: -40UP from Gibco
POLYA=No.

REFERENCE: 1 (bases 1 to 414)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy

JOURNAL (SO):

Project (CGAP), Tumor Gene Index
Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..414	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2179650" /clone-lib="NCI-CGAP-Ut2" /tissue-type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors" /lab-host="DH10B" /note="Organ: uterus; Vector: pCMV-SPORT6; Site-1: SalI; site-2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

SEQUENCE (SEQ):

1 tttgttactg attttagaaa cagtattaag caccttgggg ttttttttct gttttcaagg
61 aatgcagatt ctactaagat ctccttgcaa aatgaatgca tttatatttc cctatgtgtt
121 tttcctctgc aggtagttt cccaaagagt gctcagggtt gtaagaatga tatgggagga
181 tctcaaagag tcctggagaa acatggac tcgttccctga aggccgcgtt gaactgctca
241 gttcctggag actctcattt ttatttcaac attctccagg cagttacaga tgtgattcgt
301 atcaacgggc gtatgttgtt cctggcaac ttttctacac ttataacag gtaatcatgc
361 cctagctgtg ttgacctcat caattttcc tggcttcctt cttccagggg gttc

L4 ANSWER 80 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI384100 GenBank (R)

GenBank ACC. NO. (GBN): AI384100

GenBank VERSION (VER): AI384100.1 GI:4196881

CAS REGISTRY NO. (RN): 225337-06-4

SEQUENCE LENGTH (SQL): 547

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 28 Mar 1999

DEFINITION (DEF): te36e07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone
IMAGE:2088804 3' similar to TR:035464 035464
SEMAPHORIN ***VIA*** . ;, mRNA sequence.

SOURCE: human.

ORGANISM (ORGN): Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 131 a 119 c 119 g 178 t

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 639 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 461.

REFERENCE: 1 (bases 1 to 547)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy

Project (CGAP), Tumor Gene Index

JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..547	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2088804" /clone-lib="Soares-NhHMPu-S1" /tissue-type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab-host="DH10B" /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia)

with a modified polylinker;
 Site-1: Not I; Site-2: Eco RI;
 Equal amounts of plasmid DNA from
 three normalized libraries
 (melanocyte 2NbHM, pregnant uterus
 NbHPU, and fetal heart NbHH19W)
 were mixed, and ss circles were
 made in vitro. Following HAP
 purification, this DNA was used as
 tracer in a subtractive
 hybridization reaction. The driver
 was PCR-amplified cDNAs from pools
 of 5,000 clones made from the same
 3 libraries. The pools consisted
 of I.M.A.G.E. clones
 260232-265223, 340488-345479, and
 484488-489479."

SEQUENCE (SEQ):

```

1 caagactccg gtaaaatgact gcgtcaatgg caaggaagtc agtcaactgtg gctgagttata
61 gttttccatc tgcaaaacagt gcaacgttgg catgtttggc atcatatggg catctggcca
121 ttccgcgtaa ttcatccccg aatggttcca atgtatccat cttatagttt ctgcaggaaag
181 ggttgaaggc attagttcca cagacaaaca atgcacatc gtttttcttt agaagaactt
241 taataaaagtt gtggcactca tccttatgtt ttcccttcat tctgcatgtg tctacatcg
301 cctgtctaga tttccatgtc agtttttgc tacaataaat ttcttccgtg tgtgatgtgt
361 ctatataac agtataaaata tggtccctag cagcaatgtt gaggggttccg ttcatgtatca
421 taatcatctg gatgtccagc ctgtgcctct gtgtgggttt ccgtcctggc ttgtggccca
481 caaacaccgg atactgtttt gtatagttgc catgcgaat actgattggc tcagaatctt
541 ctggaa

```

L4 ANSWER 81 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI249189 GenBank (R)
 GenBank ACC. NO. (GBN): AI249189
 GenBank VERSION (VER): AI249189.1 GI:3844586
 CAS REGISTRY NO. (RN): 219387-10-7
 SEQUENCE LENGTH (SQL): 447
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Dec 1998
 DEFINITION (DEF): qh68h06.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo
 sapiens cDNA clone IMAGE:1849883 3' similar to
 TR:035464 035464 ***SEMAPHORIN*** ***VIA*** . ;,
 mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 109 a 95 c 89 g 154 t
 COMMENT:
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 654 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 436.
 REFERENCE: 1 (bases 1 to 447)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..447	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1849883" /clone-lib="Soares-fetal-liver-spl een-1NFLS-S1" /sex="male" /dev-stage="20 week-post conception fetus" /lab-host="DH10B (ampicillin

resistant)"
 /note="Organ: Liver and Spleen;
 Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site-1: Pac
 I; Site-2: Eco RI; This is a
 subtracted version of the original
 Soares fetal liver spleen 1NFLS
 library. 1st strand cDNA was
 primed with a Pac I - oligo(dT)
 primer [5'
 AACTGGAAGAATTAATTAAAGATCTTTTTTTTT
 TTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested
 with Pac I and cloned into the Pac
 I and Eco RI sites of the modified
 pT7T3 vector. Library went
 through one round of
 normalization. Library constructed
 by Bento Soares and M.Fatima
 Bonaldo."

SEQUENCE (SEQ):

```

1 tgttactgt tttagaaaca gtattaagca ccttgggtt ttgtttctgt tttcaaggaa
61 tgcagattct actaagatct ccttgcaaaa tgaatgcatt taattttccc tatgtgtttt
121 tcctctgcag gtagtttcc caagagtggc tcaggtttgt aagaatgata tgggaggatc
181 tcaaagagtc ctggagaaac agtggacgtc gttcctgaag gcgcgcgtga actgctcagt
241 tcctggagac ttcattttt atttcaacat tctccaggca gttacagatg tgattcgat
301 caacgggcgt gatgttgc tggcaacgtt ttctacacct tataacaggt aatcatgcc
361 tagctgtgtt gacctcatca attttccctg gcttccttct cccaaagcggtt ctttctaat
421 aaaccatatt tgcaactgac tgaaaat

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L4 ANSWER 82 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI247563 GenBank (R)
 GenBank ACC. NO. (GBN): AI247563
 GenBank VERSION (VER): AI247563.1 GI:3842960
 CAS REGISTRY NO. (RN): 219370-86-2
 SEQUENCE LENGTH (SQL): 359
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Dec 1998
 DEFINITION (DEF): qh60e03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo
 sapiens cDNA clone IMAGE:1849084 3' similar to
 TR:035464 035464 ***SEMAPHORIN*** ***VIA*** . ;,
 mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 75 a 92 c 79 g 113 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1108 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 307.

REFERENCE: 1 (bases 1 to 359)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..359	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1849084" /clone-lib="Soares-fetal-liver-spleen-1NFLS-S1" /sex="male" /dev-stage="20 week-post"

conception fetus"
 /lab-host="DH10B (ampicillin
 resistant)"
 /note="Organ: Liver and Spleen;
 Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site-1: Pac
 I; Site-2: Eco RI; This is a
 subtracted version of the original
 Soares fetal liver spleen 1NFLS
 library. 1st strand cDNA was
 primed with a Pac I - oligo(dT)
 primer [5'
 AACTGGAAAGAATTAAATTAAAGATTTTTTTTT
 TTTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested
 with Pac I and cloned into the Pac
 I and Eco RI sites of the modified
 pT7T3 vector. Library went
 through one round of
 normalization. Library constructed
 by Bento Soares and M.Fatima
 Bonaldo."

SEQUENCE (SEQ):

1 atctttctct gttgtatTTT tccgtcttgc acactcttc cttatggtga attgccttga
 61 ctgcctttta ttaccaaggg tattttttgg atcacagaat ctttatttct taagagatAT
 121 ttgctgcttc tacttaaggc acaatccTTT gtcacaggac aatcatttcc acagcaacca
 181 actgtgatgt cacaattgaa gggaggagga ccctcaaaGG ccacgaccag ctggttcccg
 241 tcaccctctt ggcatttgc a gtcattcctgg ctttcgtcat gggggccgtc ttctcgggca
 301 tcaccgtcta ctgcgtctgt gatcatcgcc gcaaagacgt gggaaaactg ggccgcgtg

L4 ANSWER 83 OF 86

GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI240716 GenBank (R)
 GenBank ACC. NO. (GBN): AI240716
 GenBank VERSION (VER): AI240716.1 GI:3836113
 CAS REGISTRY NO. (RN): 219272-64-7
 SEQUENCE LENGTH (SQL): 299
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Dec 1998
 DEFINITION (DEF): qh50a02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo
 sapiens cDNA clone IMAGE:1848074 3' similar to
 TR:035464 035464 ***SEMAPHORIN*** ***VIA*** . ;,
 mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 63 a 76 c 59 g 101 t
 COMMENT:
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1136 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 239.
 REFERENCE:
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..299	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1848074" /clone-lib="Soares-fetal-liver-spl /sex="male" /dev-stage="20 week-post"

conception fetus"
 /lab-host="DH10B (ampicillin
 resistant)"
 /note="Organ: Liver and Spleen;
 Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site-1: Pac
 I; Site-2: Eco RI; This is a
 subtracted version of the original
 Soares fetal liver spleen 1NFLS
 library. 1st strand cDNA was
 primed with a Pac I - oligo(dT)
 primer [5'
 AACTGGAGAATTAATTAAAGATCTTTTTTTTT
 TTTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested
 with Pac I and cloned into the Pac
 I and Eco RI sites of the modified
 pT7T3 vector. Library went
 through one round of
 normalization. Library constructed
 by Bento Soares and M.Fatima
 Bonaldo."

SEQUENCE (SEQ):

1 atctttctct gttgtatTTT tccgtcttgc acactcttc cttatggta attgccttga
 61 ctgcctttta ttaccaaggg tatttggat atcacagaat ctttatttct taagagatAT
 121 ttgctgcttc tacttaagtca acaatcctt gtcacaggac aatcatttcc acagcaacca
 181 actgtatgtt cacaattgaa gggaggagga ccctcaaagg ccacgaccag ctggttcccg
 241 tcaccctctt ggcattgca gtcattcgtt ctttcgtcat gggggccgtc ttctcgcca

L4 ANSWER 84 OF 86 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI122050 GenBank (R)
 GenBank ACC. NO. (GBN): AI122050
 GenBank VERSION (VER): AI122050.1 GI:3522374
 CAS REGISTRY NO. (RN): 214710-75-5
 SEQUENCE LENGTH (SQL): 163
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 2 Sep 1998
 DEFINITION (DEF): uc46b03.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA
 clone IMAGE:1401005 5' similar to TR:035464 035464
 SEMAPHORIN ***VIA*** . ;, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 27 a 43 c 51 g 42 t
 COMMENT:

Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:912721

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 1.

REFERENCE: 1 (bases 1 to 163)
 AUTHOR (AU): Marra,M.; Hillier,L.; Allen,M.; Bowles,M.; Dietrich,N.;
 Dubuque,T.; Geisel,S.; Kucaba,T.; Lacy,M.; Le,M.;
 Martin,J.; Morris,M.; Schellenberg,K.; Steptoe,M.;
 Tan,F.; Underwood,K.; Moore,B.; Theising,B.; Wylie,T.;
 Lennon,G.; Soares,B.; Wilson,R.; Waterston,R.
 TITLE (TI): The WashU-HHMI Mouse EST Project
 JOURNAL (SO): Unpublished (1996)

FEATURES (FEAT): Feature Key Location Qualifier

SEQUENCE (SEQ):

1 gatcataggg ctggagctgg acactgaggg tcacaggcct tttgtggcct ttccctggatg
61 tatacgctac ctctctctca gccgggtgtgc ccgcgtatgga gcatgtcaga ggagctgcct
121 ggcttctctg gaccctact gtggatggca tcgatccaga ggc

L4 ANSWER 85 OF 86 GENBANK. RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AA939047 GenBank (R)
GenBank ACC. NO. (GBN): AA939047
GenBank VERSION (VER): AA939047.1 GI:3098960
CAS REGISTRY NO. (RN): 207372-37-0
SEQUENCE LENGTH (SQL): 487
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 7 Jul 1998
DEFINITION (DEF): op56h03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1580885 3' similar to TR:035464 035464
 SEMAPHORIN ***VIA*** . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): *Homo sapiens*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae: *Homo*

NUCLEIC ACID COUNT (NA): 124 a 146 c 117 g 100 t

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1276 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 242.

REFERENCE: 1 (bases 1 to 487)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, cancer Project (CGAP). Tumor Gene Index

JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

FEATURES (PLAT).		Qualifier
Feature Key	Location	
source	1..487	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1580885" /clone-lib="Soares-NFL-T-GBC-S1" /lab-host="DH10B" /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Equal amounts of plasmid DNA from three

normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```

1 tttcatgcag gacattgatt tattttttca aaaagtaccc tactgtgtgc caagtactga
61 gctacatgct gggtatctgg aggtatccga ccctttccg atactcccg ggtattcaga
121 atgctgtctc gctgctgcg caggacacac actcaggat gtgggctgag caagggagg
181 tgagggtggg acaagaggac tcaccataag cagaatcccc agggccagac tgactcccg
241 tagctccatc ttggcagtca ccatgtccca tggattcccg gttcccgatcc tgatccat
301 cagtccccacc agatccccctg atatccacac agccccctgga gctatgccc catccacat
361 ggtcctgaga agccaaacag ctcctctgac agggcccatg ccgggcaaac cgctgttagag
421 ggaggttagac aatacagcca gaaaaagccc cacaaagcct gtgaccccca gtgtccagct
481 caagcccc

```

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GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF030430 GenBank (R)
 GenBank ACC. NO. (GBN): AF030430
 GenBank VERSION (VER): AF030430.1 GI:2623161
 CAS REGISTRY NO. (RN): 200046-44-2
 SEQUENCE LENGTH (SQL): 2770
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 15 Nov 1997
 DEFINITION (DEF): Mus musculus ***semaphorin*** ***VIa*** mRNA,
 complete cds.
 SOURCE:
 ORGANISM (ORGN): house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathini; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 720 a 735 c 701 g 614 t
 REFERENCE:
 AUTHOR (AU): 1 (bases 1 to 2770)
 Zhou,L.; White,F.A.; Lentz,S.I.; Wright,D.E.;
 Fisher,D.A.; Snider,W.D.
 TITLE (TI): Cloning and expression of a novel murine semaphorin
 with structural similarity to insect semaphorin I
 JOURNAL (SO): Mol. Cell. Neurosci., 9 (1), 26-41 (1997)
 OTHER SOURCE (OS): CA 127:106980
 REFERENCE:
 AUTHOR (AU): 2 (bases 1 to 2770)
 Zhou,L.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (17-OCT-1997) Neurology, Washington
 University, 660 S. Euclid Ave., St. Louis, MO 63110,
 USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2770	/organism="Mus musculus" /db-xref="taxon:10090" /clone-lib="mE10 cDNA library"
CDS	74..2740	/codon-start=1 /product="semaphorin VIa" /protein-id="AAB86408.1" /db-xref="GI:2623162" /translation="MRPAALLCLTLLCAGAGF PEDSEPIISIHSNYTKQYPVFVGH KPGRNTTQRHRLDIQMIMIMNRTLYVAARDHIYT VDIDTSHTEEIYCSKKLTWKSQRA DVDTCRMKGHKDECHNFIKVLLKKNDDTLFVCG TNAFNPSRNYRVDTLETFGDEFS

GMARCPYDAKHANIALFADGKLYSATVTDFAID
 AVIYRSLGDSPTLRTVKHDSKWLK
 EPYFVQAVDYGDIYFFFREIAVEYNTMGKVVF
 RVAQVCKNDMGGSQRVLEKQWTSF
 LKARLNCSVPGDSHFYFNILQAVTDVIRINGRDV
 VLATFSTPYNSIPGSAVCAYDMLD
 IANVFTGRFKEQKSPDSTWTPVPPDERVPKPRPGC
 CAGSSSLEKYATSNEFPDDTLNFI
 KTHPLMDEAVPSIINRPWFLRTMVRYRLTKIAVD
 NAAGPYQNHTVVFLGSEKGIILKF
 LARIGSSGFLNGSLFLEEMNVNPEKCSYDGVED
 KRIMGMQLDRASGSLYVAFSTCVI
 KVPLGRCERHGKCKKTCIASRDPYCGWVRESGSC
 AHLSPLSRLTFEQDIERGNTDGLG
 DCHNSFVALNGHASSLYPSTTSDSASRDGYESR
 GGMLDWNDLLEAPGSTDPLGAVSS
 HNHQDKKGVIRESYLSNDQLVPVTLLAIAVILA
 FVMGAVFSGIIVYCVCDHRRKDVA
 VVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKD
 PKPEAILTPLMHNGKLATPSNTAK
 MLIKADQHLDLTALPTPESTPTLQEKRKPNRGS
 REWERNQNIINACTKDMPPMGSPV
 IPTDLPLRASPISHIPSVVVLPITQQGYQHEYVDQ
 PKMSEVVAQMALEDQATLEYKTI
 KEHLSSESSSPYVLQFSEAFNRQGIILSVAVE"

SEQUENCE (SEQ):

1 agccgcggcc gcctgcccgt cgatgcacccg aaaagggtga agtagagaag caagtcccc
 61 cgctgaacct actatgcggc cagcagcctt actgctgtt ctcacactgc tacactgcgc
 121 tggggctggt ttcccagaag attccgagcc aatcagtatt tcgcacggca actataaaaa
 181 acagtatccg gtgtttgtgg gccacaagcc aggacggAAC accacgcaga ggcacaggct
 241 ggacatccag atgatcatga tcatgaacag aaccctctac gttgctgctc gagaccatata
 301 ttatactgtt gatataagaca catcccacac agaagaaaatt tactgttagca aaaaactgac
 361 atggaaatct agacaggctg acgttagacac atgcaggatg aaggggaaac ataaggatga
 421 atgtcacaac ttcattaaag ttcttctcaa gaagaatgtat gatacgtgt ttgtctgtgg
 481 aaccaatgcc ttcaaccctt cctgcagaaaa ctacagggtc gataacctgg aaacttttgg
 541 ggatgaaattt agcggaaatgg ccagatgccc ttatgatgcc aaacatgcca acatgcct
 601 gtttgcagat gaaaaactct actcggctac agtgcactgac tttctggcca ttgatgcagt
 661 catttacagg agcctcgagg acagccctac cctcaggact gtcaagcatg attcaaagt
 721 gttgaaagag cctgtactttt tccaaaggccgt ggattatggg gactataatct acttctt
 781 cagagaaat gcaatgatgaaat acaacactat ggggaagggtt gtttcccta gggtggctca
 841 ggtctgttaag aatgacatgg gagggtctca gagagtccctg gagaaggcagt ggacatctt
 901 cctgaaggct cgcctgaact gtcgggtcc tggagactct catttttatt tcaatataact
 961 ccaggcagtt acagatgtga ttgcattaa tggccgtgat gttgtcttgg caacctttc
 1021 cacacccat aacagcatcc caggttctgc agtctgtgcc tatgacatgc ttgacattgc
 1081 taatgtttc actggggaggt tcaaggaaca gaaaatcacct gactctaccc ggacaccgt
 1141 tccagacgaa cgagtcctta agcccaggcc aggctgttgc gctggatcat cctctttaga
 1201 aaaatatgca acctccaaatg agtttcccga tgataccctg aacttcattaa agacgcatt
 1261 actcatggac gaggcagttc cttccatcat caacagaccc tggttccctga gaacaatgg
 1321 cagataccgc ctgaccaaaa ttgcagtaga caacgcgtcc gggccatatac agaatcac
 1381 tggggttttc ctgggatcag aaaagggaaat catcctgaag ttcttggcca ggataggaag
 1441 cagtgggttc ctaaatggca gcctttccct ggaggagatg aatgtttaca acccagaaaa
 1501 gtgcagctat gatgggttag aagacaaaag gatcatgggc atgcagctcg acagagcgag
 1561 tggctcactc tatgttgcatt tctctacttgc tgcgtatcaag gtcgccttgc gccgcgt
 1621 gcgacatggg aagtgtaaaa aaacctgcatt cgcctccaga gaccgttatt gttgggtgg
 1681 aaggggaaagt gtttccctgtg cccatctgtc acccccttagc agactgcatt ttgagcagg
 1741 cattgagcgt ggcaataacgg acggccttagg agactgtcatt aattccctcg tggcactgaa
 1801 tgggcacgcc agttcccttct atcccagcac cactacgtca gattcggcat cccgagacgg
 1861 gtatgagtct agggggagga tgctggactg gaacgcactg ctcgaggcac ctggcagcac
 1921 agaccctttg ggggcagttgt cctctcataa ccaccaggac aagaagggag tgattcgg
 1981 aagttaccc aaaaccaacg accagcttgc tcctgtcacc ctccctggca ttgcagtcatt
 2041 tctggctttt gtcattgggg ccgtttctc gggcatcatc gtgttattgtg tgcgtatca
 2101 cccggcggaaa gacgtggcag tagtgcaggc caaggagaaaa gagtcactc actcgcgtcg
 2161 gggatctatg agcagtgtca ccaagctcg tggccttgc tggggacaccc agtccaagga
 2221 cccaaagccctt gggccatccatc tcacaccact catgcacaaac ggcaagctgg ccacgcct
 2281 caacaccggcc aagatgtcatt tcaaggctga ccagcatcatc cttagacccca cccgcct
 2341 caccggcggaaa tccaccccgaa cactgcaggc gaaacggaaa cccaaacccgcg ggagtcgc
 2401 gtgggagagg aaccagaaca tcatcaatgc ctgcaccaag gacatgcctc ccatgggtt
 2461 ccctgtgatt cccacggacc tgccccctcg ggcctccca agccacatcc ccagcgtgg
 2521 ggtccctggccc atcacgcaggc agggctacca gcacgcgtac gtatgcattc ccaaaatgag
 2581 cgagggtggg gctcagatgg cactggagga ccaggctgcc accctggagt ataagaccat
 2641 caaagagcac ctgagtagcgc agagttcacc ctatgttgc taaagcaatttt ctgaaggc
 2701 caacagacaa ggaatcattc tctccgtac ggtagaatag ctgcgtcaga tgggtgc
 2761 gcatggtaac